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(57) Abstract

The invention involves production of transgenic plants containing DNA encoding AC1/C1 wildtype and mutant sequences that negatively interfere in trans with geminiviral replication during infection. The transgenic plants produced by the invention are resistant to viral infection.

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TITLE

TRANSGENIC PLANTS EXPRESSING GEMINIVIRUS GENES

Description of Invention

A variety of geminivirus genes and mutant derivatives were generated and transferred to plant cells. Transgenic plants containing these genes were produced. Transgenic plants containing trans-dominant mutations developed resistance to geminivirus infection.

BACKGROUND

Geminiviruses present the most serious disease problem in many vegetable crops in tropical and subtropical regions. For example, major epidemics of geminivirus infections of beans and tomatoes have occurred in Florida, the Caribbean Basin, Mexico, and Central America. In the past, traditional breeding methods failed to produce cultivars with significant levels of resistance to geminiviruses. An alternative approach lies in producing virus-resistant transgenic plants according to the present invention.

The geminivirus group are single stranded DNA viruses that infect both monocotyledonous (monocot) and dicotyledonous (dicot) plants. A common feature among all gemini viruses is the mode of genomic replication, which involves a rolling circle mechanism.

Tomato mottle virus (ToMoV) is one example of a geminivirus. It has a two component (bipartite) genome, an ability to infect dicot plants and is transmitted by whitefly. The DNA of its two genomic components, DNA-A and DNA-B, has previously been cloned and sequenced. Isolated clones of DNA-A and DNA-B of ToMoV are themselves infectious when mechanically inoculated into tomato and *N. benthamiana*, or when delivered to either host by agroinoculation. An invariant geminiviral DNA sequence required for replication is present in an intergenic, common region (CR) in each genomic component.

The ToMoV DNA-A genomic component has four ORF, one of which, AC1, must be expressed for efficient replication of both A and B components. The AC1 ORF encodes a protein having several functional activities: a DNA binding site specific to the DNA-A CR; a DNA nicking activity; and a NTP binding activity. The DNA binding region mediates an initiator protein function during rolling circle replication.

AC3 protein is a second ToMoV-coded function involved in DNA replication and production of single-stranded circular DNA.

Tomato yellow leaf curl virus (TYLCV) is another example of a geminivirus. TYLCV has a monopartite genome organization, infects monocot plants, and is leaf-hopper transmitted. The TYLCV C1 protein is required for replication, encoded by the C1 ORF.

Being DNA viruses, geminiviruses offer advantages for antiviral strategies. Several geminiviruses have been cloned and sequenced. Transgenic plants having mutant viral genes can be produced, e.g., by introducing expression cassettes comprising mututated virus genes directly into plants with a particle gun, or into plant suspension cells or protoplasts by electroporation, or by Agrobacterium transfection.

Summary Of The Invention

The invention involves production of transgenic plants containing DNA encoding AC1/C1 wildtype and mutant sequences that negatively interfere in trans with geminiviral replication during infection. The resulting transgenic plants are resistant to viral infection.

Description of the Figure

Fig. 1 shows the results of a transient assay for trans-dominance done with BGMV-GA in NT-1 cells.

Detailed Description Of The Invention

A. Production of infectious clones

Infectious clones of geminiviruses are produced by methods known to the skilled worker. Geminivirus DNA is extracted from tissue as follows. Young tissue is collected from infected plants, frozen in liquid nitrogen and ground in a mortar in the presence of extraction buffer (10 mM Tris-Cl, pH 7.5, 10 mM EDTA, and 1% SDS, 1:4 wt/vol ratio) and centrifuged for about 10^3 g minutes. The supernatant is adjusted to about 1 M NaCl and stored at about 4°C for about 12 hr, then centrifuged for about 10^7 g minutes. After phenol extraction, the solution is adjusted to 0.3 M sodium acetate, and the DNA is precipitated in alcohol. Viral nucleic acids are isolated by agarose gel electrophoresis.

These viral nucleic acid fractions are digested with restriction enzymes and isolated by agarose gel electrophoresis. The DNA is cloned in a suitable cloning vector, e.g., pBluescript KS+, and its identity is confirmed by sequencing.

Full-length clones of the geminivirus genome are constructed, e.g., by a PCR-based cloning strategy. Primers are synthesized that will amplify the entire ORF plus about ten nucleotides on each side of the ORF. The primers should include mismatched bases to create restriction sites before and after the C1 or AC1 ORF which will allow convenient cloning without altering initiation and termination codons of C1 or AC1 ORFs.

Primer 1 is complementary to and anneals with the viral sense strand of the geminiviral genome. The 5' end of the primer is located 40-50 base pairs 3' of the translation start, and the 3' end is located 10-20 base pairs 3' of the translation start site. Translation start is defined by CAT on the viral sense strand; AC1 or C1 ORFs are located on the complementary strand of the viral genome and sequence coordinates are given for the viral sense polarity strands.

Primer 2 is complementary to and anneals with the strand (complementary sense polarity) of the geminiviral genome. The 5' end of the primer is located 40-50 base pairs 3' of the AC1 or C1 termination condon, and the 3' end of the primer is located 10-20 base pairs 3' of the translation stop as determined on the complementary sense polarity strand.

The primers are used in a PCR reaction to amplify the C1 or AC1 ORF from cloned viral DNA or purified geminivirus DNA. The amplified DNA is digested with appropriate restriction enzymes to cut sites engineered in the ends of the PCR fragment and the resulting fragment is cloned into a suitable vector. C1- or AC1-

containing clones are identified and sequenced to confirm the presence and integrity of the cloned C1 or AC1 ORF.

The sequence of the AC1/C1 ORF is used for designing the primers for amplification of the PCR fragment of AC1/C1 ORF. For example, these primers are designed so that this ORF is cloned into the BamHI and HindIII sites of pBluescript KS+. The BamHI site is located at the 5' end of the complementary sense primer, which amplifies the amino terminal end of the ORF. A HindIII site is located at the 5' end of the viral sense primer which anneals to the carboxy end of the ORF.

Infectious clones preferably are selected. The infectivity of the clones are determined by construction of *Agrobacterium* having greater-than-full-length viral genes with at least two common regions of DNA-A and DNA-B. Infectivity is determined by microparticle inoculation. Seeds are germinated on moist filter paper to produce 1-3 cm long radicles of a host, and this tissue is bombarded by DNA-coated particles with a particle gun. Inoculated plants are placed in a growth chamber at about 26°C with about 14 hour photoperiods. Infectivity is confirmed by PCR with primers specific for geminiviruses or Southern blot analysis. For example, 1.3-kb PCR products are expected when primers PAL1v1978 and PAV1c715 are used.

Cloned viral DNA is digested with restriction enzymes and analyzed on agarose gels to produce a unique 2.5 to 2.7-kb fragment. The DNA bands are removed from the gel and cloned into an appropriate vector. For monopartite geminiviruses, the insert preferably includes the entire genome. For bipartite geminiviruses, entire inserts of both genomic components are preferable. The single insert of the monopartite geminivirus or both cloned components of bipartite geminiviruses are introduced into a host

plant and tested for infectivity by biolistic delivery or agroinoculation.

The cloned C1 (monopartite viruses) or AC1 (bipartite viruses) ORF are isolated by selecting for the following characteristics:

A. The AC1 or C1 ORF encodes a protein product of about 42 Kd.

B. The nucleotide sequence of the C1 or AC1 ORF is at least 60% homologous to the AC1 ORF of a previously identified geminiviruses (e.g., BDMV, ToMoV, or TYLCV). The deduced amino acid sequence of the ORF will contain several characteristic sequences which are similar in sequence and relative position within the ORF i.e., motifs within the C1 or AC1 sequences.

B. Introducing Mutations

Mutations are introduced by site-directed mutagenesis of cloned C1 or AC1 ORF by methods known in the art, e.g., using the method of Kunkel et al. (Recombinant DNA Methodology, 1989, pp. 587-601) (herein, "Kunkel mutagenesis").

In particular, mutations are introduced into amino acid sequence motifs in C1 or AC1 ORF that are highly conserved among all gemini viruses. Four motifs are preferred in the DNA-nicking domain of the protein. These include (capital letters denote high conservation of amino acid, lower case denotes some conservation, and "x" denotes a variable position in the motif):

(1) FLTYpxC

(2) HlHvliQ

(3) vKxYxdKd; and

(4) FHPNIQxak.

Additionally two motifs are preferred in the NTP-binding domain of the protein. These include:

(5) EGx_2RTGKt; and

(6) NviDDi.

The individual codons specifying the most highly conserved amino acids within these motifs are mututated. For example, one or more of the following mutations introduced to the C1 or AC1 ORF:

(1) vKxYxdKd to (a) vKxFxdKd;
(b) vKxAxdKd;
(c) vKxYxdRd;

(2) EGx_2RTGKt to (a) EGx_2RTGHt;
(b) EGX_2RTGAt;
(c) $RGx_2RTGKht$;

(3) NviDDi to (a) NviRDi;
(b) NviKDi; or
(c) NviDYi,

(herein mutations 1(a), 1(b), 1(c), 2(a), 2(b), 2(c), and 3(a), 3(b), 3(c), respectively). Acidic or basic amino acids are changed to the opposite charge, to alanine (alanine scanning) or to other neutral amino acids. Combinations of mutants are also made. For example, a single C1 or AC1 ORF containing codon changes corresponding to vKxFxdKd and EGx_2RTGHt (double mutations 1(a) and 2(a), above) are constructed and

tested. Other mutants in motifs within AC1/C1 are possible and are used. The presence of the codon change is confirmed by DNA sequencing. *Agrobacterium*-mediated transfer of the plant expressible mutated AC1/C1 ORF is done using procedures known to those skilled in the art.

If an infectious clone of the geminivirus is available, effects of mutations on replication can be tested. The mutation is introduced into the C1 or AC1 ORF of an infectious clone. Mutant DNA is transferred to plant cells. Replication of wild type viruses is tested for infection as a positive control. Mutations which create transdominant molecules generally abolish replication when engineered into infectious clones. A number of mutations which change codons for conserved amino acids within these motifs will be lethal and potentially transdominant. Other mutations in C1 or AC1 which abolish replication should also be considered potentially transdominant. Any non-functional C1 or AC1 molecule has the potential to be transdominant.

Mutated C1 or AC1 ORFs are installed into a suitable plant transformation vector in the sense orientation and under the control of a strong constitutive promoter sequence and suitable terminator for high level expression in the target plant species. This step is performed for each of the C1/AC1 mutants created.

C. Assays

A transient assay is useful to screen candidate constructs for transdominant interference activity. This is done by first coinoculating protoplasts or a plant cell suspension culture with the infectious geminivirus clone and a plasmid containing mutant C1 or AC1 ORF under control of a strong constitutive plant promoter. Control treatments are inoculated with an infectious clone. Total DNA is harvested from inoculated cells, and is assayed for viral replication. Transominant C1 or AC1 mutants are identified as those which suppress geminiviral replication relative to control treatments after coinoculation.

In vitro assays for transdominance correlate lethal mutations and transdominant activity in transient assays. This is exemplified in a BGMV-GA model system. These results are readily applicable to produce a transdominant C1 or AC1 ORFs from other geminiviruses. Transgenic plants resistant to ToMoV were created by transforming them with an AC1 ORF derived from ToMoV and engineered to contain similar mutations.

Expression cassettes constructed above are installed into binary plasmids and transformed into *Agrobacterium* strains for plant transformation protocols. Plants are transformed by methods tailored to the specific variety or line.

Transgenic status of R_0 and later generation plants and their segregating progeny is verified by routine methods, including: ELISA assays for NPTII protein detection; DNA assays such as PCR amplification with the AC1/C1 primers of plants and Southern blot hybridization for detection of transgenes using AC1/C1 as viral probes; and Southern blot hybridization to detect ACI or CI transgenes. Demonstration that R_1 plants transformed with geminivirus gene constructions express NPTII protein is done by ELISA. Protein in leaf tissue samples taken from R_1 transgenic plant seedlings is extracted and analyzed for NPTII protein by ELISA.

Geminivirus transgene expression is also measured by Northern blot analysis. Transgene expression in a number of R_0 and R_1 plants was done by Northern blot hybridization. Total RNA extracted from leaves of transgenic plants is separated by agarose gel electrophoresis. After electrophoresis, RNA is pressure blotted onto membrane. Membranes are hybridized with radiolabeled probes, washed, and autoradiographed.

D. Identification of gemini-resistant transgenic plants

Geminivirus-resistant transgenic plants are identified by challenging transgenic plants and progeny. R_1 plants from self pollinated R_0 primary regenerants are

agroinoculated about 3 weeks after sowing. Alternative methods include biolistic inoculation, sap transmission from infected tissue (if the isolate is mechanically transmissible), insect transmission, or grafting. For bipartite geminiviruses, agroinoculation preferably involves delivery of greater-that-full-length (i.e., at least 2 common regions) DNA-A and DNA-B components into the seedlings using *Agrobacterium* strains, e.g., containing a binary vector having in its T-DNA a partial or full tandem duplication of infectious geminivirus DNA. Geminivirus-resistant plants are incorporated into traditional breeding programs to develop elite breeding lines that include the resistance-conferring transgene. These changes produce C1 or AC1 molecules when made alone or in combination with a mutant.

Plants showing the highest steady state levels of transgene RNA are challenged by *Agrobacterium*-mediated inoculation. Resistance is determined by lack or delay of symptom expression and low levels of viral DNA in plants as determined by squash blot hybridization tests with viral probes (Gilbertson et al., 1991. Plant Disease 75:336-342.). Resistance is also determined by inoculation with viruliferous *Bemisia tabaci* as described. It is expected that plants with low levels of mRNA accumulation for the mutated AC1/C1 ORF have symptoms and those with high levels have no symptoms.

Since the AC1/C1 proteins have domains required for DNA-nicking and NTP-binding that are conserved among all geminiviruses, an antiviral strategy involving mutated AC1/C1 protein is applicable to plant-geminivirus systems in general.

Other viruses include:

Virus	Genes/Regions	SEQ ID NO.
TGV-GA1	AC1 ORF DNA-A (complementary seq)	57
TGV-GA1	Common & Intergenic Region (viral)	58
TLCV-IND	Full Length Sequence (stemloop begin)	59
"Chino"	Partial AC1, Common region, AV1	60
PHV	AC1, Common region, Intergenic, AV1	61
PHV	BV1 ORF	62
PHV	BC1, Hypervar., Common, & Interg. Reg	63

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1. **Gene Expression Vectors**

All *E. coli* culture and plasmid DNA isolation methods were carried out according to standard methods. Restriction digestions, filling in of 5' end overhangs, calf intestinal alkaline phosphatase treatments of DNA and ligation of DNA fragments and gel electrophoretic separation of DNA fragments and their isolation from gels were done according to manufacturers'

recommendations and methods. *Agrobacterium* large plasmid DNA was isolated. *Agrobacterium* transformation and culture is performed according to general methods known to those skilled in the art.

Tables 1A and 1B list geminiviral transcribed sequences, expression vectors, binary plasmids, and *Agrobacterium* strains described in the Examples.

Tabl 1A. Constructs used to Creat Transgenic Plants

Transcribed Seq. (open reading frame or antisense seq.)	Expression Vector Used	Binary Vector Used	*Agrobacterium tumefaciens* designation
ToMoV-AC1*as*	pRT101e	pJTS246Δ	RTAC
ToMoV-AC1	pRT101e	pJTS246Δ	RTSC
ToMoV-AC1*as*	DH51	pJTS235	DHAC
ToMoV-AC1	DH51	pJTS235	DHSC
ToMoV-AC1-AC2-AC3*as*	pRT101e	pJTS246Δ	RT3AA
ToMoV-AC1as	pRT101e	pJTS246Δ	RTFS
ToMoV-AC1	pLAT	pJTS246Δ	LASD, LASU
ToMoV-AC1dlm	pRT101e	pJTS246Δ	MEU
ToMoV-AC1dlm	pRT101e	pJTS246Δ	MEU2
ToMoV-AC1dlm1	pRT101e	pJTS246Δ	MUA
ToMoV-AC1dlm23	pRT101e	pJTS246Δ	MUB
ToMoV-AC1	pΔ1CO35	pJTS246Δ	COALS
ToMoV-AC1dlm	pΔ1CO35	pJTS246Δ	CODLM
ToMoV-AC1dlm1	pRTIN	pJTS246Δ	MUAIN
ToMoV-AC1dlm23	pRTIN	pJTS246Δ	MUBIN
TYLCV-C1*as*	pRT101e	pJTS246Δ	LCA
TYLCV-ΔC2*as* TYLCV-C1*as*	pRT101e	pJTS246Δ	LCR'
TYLCV-V1*as*	pRT101e	pJTS246Δ	LCR"
TYLCV-C1-ΔC2-ΔC3*as*	pRT101e	pJTS246Δ	RT3CA
TYLCV-C1-ΔC2-ΔC3*as*	pΔ1CO35	pJTS246Δ	CO3CA
TYLCV-C104	eP_{35s}-T_{pea}	pGA482Δ+HYG^R	C104
TYLCV-C225	eP_{35s}-T_{pea}	pGA482Δ+HYG^R	C225
TYLCV-C259	eP_{35s}-T_{pea}	pGA482Δ+HYG^R	C259
TYLCV-C1-ΔC2-ΔC3	pRT101e	pJTS246Δ	RT3CS

Table 1B. Constructs for *Agrobacterium* Inoculation

Geminivirus strain and Sequence	Binary Vector Used	Agrobacterium Designation
ToMoV-A dimer	pJTS222	A.t. ToMoV-A
ToMoV-B 1.67mer	pJTS222	A.t. ToMoV-B
TYLCV-EG dimer	pJTS222	A.t. TYLC-EG

Example 1.1 **Synthesis of expression vector pRT101e**

The pRT101e expression vector listed in Table 1A was made by removing a 325-bp HindIII-EcoRV fragment from pUC8-CaMVCAT (Pharmacia) and inserting it into HincII-HindIII-digested pRT101 (Dr. Topfer, Max Planck-Institut fur Zuchtungsforschung, 5000 Koln 30, Germany), thereby adding a segment of the 35S promoter containing the upstream enhancer (Kay et al., Science, 1987, 236:1299-1302) to the 5' end of the 35S promoter sequence of PRT101.

Example 1.2 **Expression vector pDH51**

The pDH51 expression vector of Table 1A (T. Hohn, Friedrich Miescher Institute, P.O. Box 2543, CH-4002, Basel, Switzerland) is comprised of a CaMV 35S promoter-35S terminator expression cassette.

Example 1.3 **Synthesis of expression vector pΔ1CO35**

The pΔ1CO35 expression vector of Table 1A was derived from pCO1bam (Dr. Neil Olszewski, University of Minnesota-Twin Cities, College of Biological Sciences). The 1.0-kb EcoR1-SalI fragment of pCO1bam, containing the promoter controlling expression of the commelina yellow mottle virus (CoYMV) transcript (Medberry et al., Plant Cell, 1992, 4:185-92), was inserted into EcoR1-SalI-digested pSL1180 (Pharmacia). A 1.1-kb EcoRI-DraI fragment of the resulting construct was inserted into EcoRI-HincII-digested pRT101, thereby replacing the CaMV 35S promoter of pRT101 with the CoYMV promoter. Some restriction sites, including BamHI and BglII, were removed by partially digesting this plasmid with HindIII and recircularizing it with T4 DNA ligase to produce pΔ1CO35.

Example 1.4 **Synthesis of expression vector pRTIN**

The pRTIN expression vector of Table 1A is a derivative of pRT101e and pCOIN, in which the 35S terminator of pRT101e was replaced with the protease inhibitor gene terminator/polyadenylation site (T_{INH}) of pCOIN. To

produce pCOIN, the 760-bp HindIII-XbaI fragment of pTPI-1 (Dr. C. Ryan, Washington State University, Pullman, WA) containing T_{INH} was inserted into HindIII-XbaI-digested Bluescript II KS+ (Stratagene). The 770-bp XbaI-KpnI fragment of the resulting construct was inserted into XbaI-KpnI-digested pUC19. The 800-bp PstI-KpnI terminator fragment of the resulting plasmid was ligated with the KpnI-PstI fragment of pA1CO35 to produce pCOIN. The 805-bp SphI-SspI fragment of pCOIN was inserted into SphI-SmaI-digested pRT101e, thereby replacing the 35S terminator of pRT101e with T_{INH}. The resulting plasmid was further modified by inserting into a EcoRI site a DNA fragment with EcoRI ends and internal restriction sites including BamHI to produce pRTIN.

Example 1.5 **Synthesis of expression vector eP_{mas}-T_{plus}**

The expression vector eP_{mas}-T_{plus} of Table 1A was assembled by combining an octopine synthase upstream activating sequence (*ocs* UAS) and a mannopine synthase promoter (*mas2'*).

The *ocs* UAS was excised from pAL1050 (Dr. Paul J.J. Hooykaas, State Univ. of Leiden, 2333 AL Leiden, The Netherlands), which was isolated from *Agrobacterium tumefaciens* strain LBA4404 (Dr. P.J.J. Hooykaas). A 2.8-kb EcoRI fragment of pAL1050, containing nt 13362-16202 of *ocs* UAS was inserted into the EcoRI site of pSL1180 (Pharmacia). A 311-bp SacI-BamHI fragment of the resulting plasmid, containing nt 13774-14085 of the *ocs* UAS, was ligated into SacI-BamHI-digested pBluescript II KS+. A 285-bp XhoI-MfeI fragment containing the *ocs* UAS was ligated with the EcoRI-XhoI fragment of pBluescript II KS+ with *ocs* UAS to produce a plasmids having tandemly rep ated *ocs* UAS element structure. A EcoRI-XhoI fragment of the recombinant plasmid was ligated with another MfeI-XhoI fragment to

produce a recombinant plasmid, pBluescript+UAS^3, having three tandemly repeated *ocs* UAS elements.

The *mas2'* promoter element was isolated as follows. Plasmid pE93 (Dr. Stan Gelvin, Purdue University) is derived from pRK290 (Ditta et al., 1980). EcoRI fragment #13 of pE93 contains nt 16202-21634 of the octopine Ti plasmid, and lacks an internal ClaI fragment at nt 8672-20128 (Eco13ΔCla). A 4-kb EcoRI-XhoI fragment was ligated with the SalI-EcoRI fragment of pBR322, to produce pJTS213. This plasmid was introduced into *E. coli* GM119 (Dr. Gurnam Gill, Pharmacia & Upjohn, Kalamazoo, MI), which is deficient in DNA adenine methylation. Thus, normally undigestible ClaI site beginning at nt 20128 in Eco13ΔCla is cleavable by ClaI. A 951-bp ClaI-NcoI fragment of pJTS213 containing nt 21079-20128 was isolated and ligated with the ClaI-NcoI fragment of pSL1180 to produce pSL1180+P_{mas}.

A *ocs* UAS-enhanced mannopine synthase promoter cassette (Ep_{mas}) was assembled as follows. A 365-bp ClaI-FspI *mas2'* fragment from pSL1180+P_{mas} was ligated with the ClaI-EcoRV fragment of pBluescript + VAS^3. Clones in which the *mas2'* was inserted downstream of the *ocs* UAS repeat were identified by restriction digestion. To facilitate the addition of the phaseolin transcription terminator, a 250-bp multiple cloning site (mcs) XhoI-SalI fragment from pSL1180 was ligated into the XhoI-digested recombinant plasmid. Two plasmids, pBluescript+UAS^3+P_{mas}+mcs (orientations I and II), containing a construct with the mcs inserted in the two possible orientations were isolated.

The phaseolin terminator was added to pBluescript+UAS^3+P_{mas}+mcs, completing the assembly of Ep_{mas}-mcs-T_{phas}, as follows. A 1.1-kb PstI-EcoRI fragment of pUC19-*hph*-T_{phas} (described below in the assembly of pGA482Δ+HYG^R), which contains the phaseolin

transcription terminator (T_{pha5}), was ligated with PstI-EcoRI-digested pBluescript II KS+. A 1.2-kb SacII-ClaI fragment of the resulting plasmid was ligated with the SacII-ClaI fragment of pBluescript+UAS^3+P_{mas}+mcs (orientation I) to produce a plasmid having the eP_{mas}-T_{pha5} insert.

Example 1.6 **Synthesis of expression vector pLAT**

The expression vector pLAT of Table 1A was produced as follows. The promoter of the LAT52 gene (Twell et al., Development, 1990, 109:705-13) was used to construct an AC1 gene construct in sense orientation that does not express in vegetative tissue. A 600-bp NcoI-SalI fragment of pLAT52-7a (Dr. S. McCormick, Plant Gene Expression Center, USDA ARS, Albany, CA), which contains the LAT52 promoter, was ligated with NcoI-SalI-digested pSL1180 to produce pLAT.

Example 2.1 **Synthesis of binary vector pJTS246Δ**

The binary vector pJTS246Δ of Table 1A was produced as as a derivative of pGA482 (Dr. G. An, Washington State University, Pullman, WN), by replacing the nopaline synthase controlled NPTII sequence with a CaMV 35S promoter-NPTII-phaseolin terminator selectable marker. The selectable marker was situated at the left T-DNA border to insure that the passenger gene, inserted at the right T-DNA border, would be transferred into the plant cell.

A BamHI fragment of pUC8-CaMVCAT was ligated with a 2.2-kb BamHI fragment of pDOB513ro4.6K (J.L. Slightom, Pharmacia & Upjohn), containing the NPTII coding region and octopine Ti plasmid T-DNA ORF No. 26 transcription terminator, to produce pJTS228. The pJTS228 construct has the 2.2-kb fragment, inserted as a transcription fusion unit immediately downstream of the CaMV 35S promoter of pUC8-CaMVCAT. Most of the CAT gene of pUC8-CaMVCAT was deleted from pJTS228 by digesting with EcoRI to produce pJTS228Δ. A 4.0-kb BamHI-NcoI

fragment from pJTS228 was ligated with a 1.55kb BamHI-NcoI fragment from pkanPhas (J.L. SLightom, Pharmacia & Upjohn) containing the NPTII coding sequences 5' distal to the NcoI site and the phaseolin terminator. A resulting plasmid, in which the T-DNA transcription terminator fused to the NPTII ORF was replaced with the phaseolin storage protein terminator from *Phaseolus vulgaris*, was designated pJTS233.

pJTS233 was digested with HindIII and flush ended. A 2.8-kb EcoRI fragment containing the 35S promoter, NPTII coding region and phaseolin terminator was isolated and ligated in a 3-part reaction with SmaI-BamHI fragment of pUC9 and an 8.0-kb BamHI-EcoRI fragment of pGA482 containing the broad host range replicon, left and right nopaline Ti T-DNA borders and nopaline synthase promoter. The desired construct, pJTS246, was cloned and isolated. pJTS246 was modified to eliminate the ampicillin drug resistance contributed by pUC9. The plasmid was digested with ScaI and HindIII, and treated with HindIII linkers followed by HindIII digestion. The resulting plasmid, pJTS246Δ, had 1730-bp of pUC sequence deleted from pJTS246.

Example 2.2 **Synthesis of binary vector pJTL222**
pJTS222 is pGA492 (Dr. G. An) in which a 2.2-kb BamHI-HindIII fragment replaced by the 430 bp BamHI-HindIII fragment of pUC8-CamVCAT containing the CaMV 35S promoter.

Example 2.3 **Synthesis of binary vector pJTS235**
pJTS235 was a binary plasmid derived from pGA492 in which the NPTII coding sequence and its transcription terminator were removed and replaced with a CaMV 35S promoter-NPTII coding sequence-phaseolin terminator selectable marker. pJTS235 was constructed by ligating a 2.1-kb BamHI fragment of pJTS233 containing the NPTII coding sequence and phaseolin terminator into the BamHI fragment of pJTS222. The resulting plasmid, pJTS235

had the NPTII structural gene under the control of 35S promoter.

Example 2.4 **Synthesis of binary vector pJTS250**

pJTS250 was assembled as follows. A 353-bp PstI-BamHI fragment of pLG90 (provided by Dr. L. Gritz, Biogen, S.A., 46 Route des Acacias, Geneva, Switzerland), which includes the entire hygromycin phosphotransferase gene (hph) coding region from the ATG translation start codon to 15 bp distal to the translation terminator, was ligated with the PstI-BamHI digest of pUC9 to produce pUC9+*hph*-a. Another aliquot of AvaI-digested pLG90 with AvaI flush ended. The 670-bp PstI fragment was cloned into the SmaI-PstI fragment of pUC9 to produce pUC9+*hph*-b, creating a 670-bp fragment PstI-EcoRI fragment. A 1.18-kb NaeI-BamHI fragment containing the phaseolin terminator (J.L. Slightom) was cloned into the BamHI-SmaI fragment of pUC9 to create pUC9+T_{phas}. The above three fragments (353-, 670- and 1180-bp) were ligated with the BamHI digest of pJTS222. The resulting binary plasmid, pJTS250, was produced comprised of a P_{35S}-*hph*-T_{phas} plant selectable marker, and the capability to transform plant tissue to hygromycin resistance via *Agrobacterium*-mediated gene transfer.

Example 2.5 **Synthesis of binary vector pGA482Δ+HYG^R**

pGA482Δ+HYG^R was produced from the following plasmids: pGA470 (Dr. G. An); pJTS262, including the entire T-DNA of pGA470 and a broad host range replicon; pJTS222; pJTS250, a binary plasmid that includes HYG^R constructed by ligation of four fragments, including 353-bp PstI-BamHI fragment encoding part of the *hph* coding region, 670-bp PstI fragment encoding the remainder of the *hph* coding region, 1180-bp NaeI-BamHI fragment constituting T_{phas} and pJTS222 digested with BamHI; pUC19B2-P_{ocs}; pUC19B2+*hph*-T_{phas}; p_{ocs}-*hph*-T_{phas} expression cassette; and pGA482G (Dr. G. An).

The pGA482Δ+HYG^R was constructed as follows: SalI fragments of pGA470 were ligated into SalI-digested pBR322. The resulting construct, pJTS262, is comprised of the entire T-DNA of pGA470 (from right to left border) and a second fragment containing part of the broad host range replicon. The 345-bp BclI-BamHI fragment of the resulting plasmid, having the nopaline synthase promoter (P_{nos}) fused to the 5' 42-bp of nopaline synthase (14 N-terminal amino acids), was inserted into the BamHI site of pUC19B2, having the SmaI site of pUC19 converted to a BglII site. The resultant recombinant plasmid, pUC19B2+P_{nos}, had the P_{nos} segment within the BamHI-BglII fragment.

A 2.2-kb BamHI fragment containing the *hph* coding region from bacterial transposon Tn5 and the phaseolin transcription terminator (*hph*-T_{phas}) was isolated from pJTS250. The 2.2-kb *hph*-T_{phas} fragment was inserted into the BamHI site of pUC19B2. The pUC19B2-P_{nos} was digested with BamHI and HindIII. pUC19B2+*hph*-T_{phas} was partially digested with BamHI and completely with HindIII to produce a 2.2-kb fragment with BamHI-HindIII ends. The fragment was ligated with BamHI-HindIII digested pUC19B2-P_{nos} plasmid. The resulting construct, a P_{nos}-*hph*-T_{phas} expression cassette, pUC19B2+HYG^R, was partially digested with BamHI; a resulting 5.3-kb fragment was digested with BglII to produce a 2.6-kb fragment. Separately, HindIII-EcoRI-digested pGA482 was ligated with HindIII-EcoRI-digested pSL1180, lacking a mcs. The resulting construct was further restricted to delete 2.5-kb of the original T-DNA containing the mcs. This binary was digested with BglII and ligated with the BamHI-BglII-ended 2.6-kb P_{nos}-*hph*-T_{phas} fragment to produce pGA482Δ+HYG^R.

Example 3 Geminivirus DNA Insertion into Expression Vect r Constructs

Example 3.1 Synthesis of Wild-Type ToMoV-FL AC1 ORF

ToMoV was collected from infected tomato plants in Bradenton, Florida and inoculated into *Nicotiana benthamiana* and tomato. DNA was isolated from infected plants and viral DNA was isolated by preparative agarose gels. Viral DNA was digested with BglII, inserted into BglII-digested pSP72 to produce a full-length A-component clone (Seq ID 17). Similarly, a full-length DNA-B clone was produced from viral DNA digested with BamHI and inserted into BamHI-digested pBluescript II KS+ (Seq ID 18). DNA of either clone inoculated into *N. benthamiana* produced symptoms similar to the original virus.

A dimer clone in which DNA-A was inserted as a direct, tandem duplicate into the cloning vector was made by removing the single insert from its original vector with BglII and reinserting it into BglII-digested pSP72. The ApaI fragment of the resulting plasmid comprising the cloned DNA-A was inserted into the ApaI site of pBluescript II KS+.

Example 3.3 Synthesis of ToMoV-AC1

Wild type AC1 sense ORF and antisense (as) ORF of Table 1A were constructed from the AC1 ORF (SEQ ID 1 and 2) and part of the intergenic region was amplified by PCR from ToMoV-infected *N. benthamiana* DNA using primers PFL-2549B (SEQ ID 9) (5'-GGATCCGAGTAACTCATCTGGAGTACC-3') and PFL-1108B (SEQ ID 10) (5'-GGATCCGGAAGTAGATGGAGCACCCGC-3'). The 1.1-kb PCR product was BamHI-digested and inserted into the BamHI site pBluescript II KS+ to produce pTFAC1.

Example 3.4 **Synthesis of ToMoV-AC1dlm**

For the production of the mutated ORF, the AC1 ORF and part of the intergenic region was PCR amplified from ToMoV-infected *N. benthamiana* DNA by PCR using primers PFL-2549H (SEQ ID 16) (5'-TATCAAAGCTTGAGTAACTCATCTGGAGTACC-3') and PFL-1108B (SEQ ID 10) (5'-TATCGGATCCGGAAGTAGATGGAGCACCCGC-3') to produce a HindIII site near the translation start codon and a BamHI site near the translation terminator codon. The HindIII-BamHI-digested product was ligated with HindIII-BamHI-digested pBluescript II KS+ in a sense orientation relative to the f1 origin of replication. Mutations were generated in the NTP binding motifs of AC1 of this clone.

Trans-dominant lethal mutants (dlm) of AC1 protein (SEQ ID 3 and 4) were created by Kunkel mutagenesis. The above pBluescript plasmid was transformed into CJ236 (Invitrogen Co.), a *dut-*, *ung-* strain, so that the amplified plasmid DNA contains uracil. Single-stranded DNA was produced by transfecting the above transformed cells with helper phage M13-K07. The complementary sense strand of the ssDNA was synthesized in vitro using deoxynucleotides, including dTTP, and two mutagenic primers: PFAC1-680c (SEQ ID 11) (5'-CAAGAACAGGGcAcACGATGTGGG-3') and PFAC1-781c (SEQ ID 12) (5'-GTATAACGTCATTaAatACATCGCACCGC-3'). The lower case letters indicate altered nucleotides. The product was treated with T4 DNA ligase and transformed into XL1 Blue *E. coli* (Stratagene) to amplify plasmids containing the mutations produced by the mutagenic primers, which resulted in the mutations 2(a), 3(b) and 3(c), described above.

Example 3.5 **Synthesis of ToMoV-AC1dlm1**

The 1.1-kb BamHI fragment of pTFAC1, containing wild type AC1 ORF, was inserted to the BamHI site of pRT101e to produce a sense (pRTAC1-S) construct. The AC1 triple mutant (AC1 dlm) ORF was removed as a 1.1-kb

XhoI-BamHI fragment from its vector and inserted in the sense orientation into XhoI-BamHI-digested pRT101e to produce pRT101e+AC1dlm. Plasmids pRTAC1-S and pRT101e+AC1dlm were cleaved at the unique PmlI site. After an additional digestion with ScaI, 1.6- and 3.2-kb fragments were isolated from each digest. The 1.6-kb fragment from pRTAC1-S was ligated with the 3.2-kb fragment from pRT101e+AC1dlm to produce a construct comprising the sequence designated as ToMoV-AC1dlm1 (SEQ ID 5 and 6) in Table 1A, mutation 2a described above.

Example 3.6 **Synthesis of ToMoV-AC1dlm23**

Plasmids pRTAC1-S and pRT101e+AC1dlm were cleaved at the unique PmlI site. After an additional digestion with ScaI, 1.6- and 3.2-kb fragments were isolated from each digest. The 3.2-kb fragment from pRTAC1-S was ligated with the 1.6-kb fragment from pRT101e+AC1dlm to produce a construct comprising the sequence designated as ToMoV-AC1dlm23 (SEQ ID 7 and 8) in Table 1A, double mutations 3(b) and 3(c) described above.

Example 3.7 **Synthesis of ToMoV-AC1-AC2-AC3**

A construct containing the AC1-AC2-AC3 fragments was produced by ligating a BamHI-HindIII fragment of a binary plasmid comprised of a dimer of the full-length, infectious ToMoV A-component with BamHI-HindIII-digested pJTS222. The BamHI-HindIII fragment from this construct was inserted into BamHI-HindIII-digested pBluescript II KS+. A 1.24 kb BglII-SphI fragment of the resulting plasmid, containing the complete AC2 and AC3 coding sequences and the C-terminal two-thirds of the AC1 ORF (SEQ ID 15), was ligated into BglII-SphI-digested pSL1180. The resulting plasmid contained the ΔAC1-AC2-AC3 fragment from ToMoV-A.

Example 4. **TYLCV-IS-EG Wild Type and Mutant Sequences.**

Example 4.1 **Synthesis of TYLCV-C1**

Tomato leaves with TYLCV symptoms were collected in Fayoum, Giza and Ismailia, Egypt. They were grafted to Geneva 80 tomatoes and *N. benthamiana*. The tomatoes and tobacco developed symptoms typical of TYLCV. Infectious TYLCV (TYLCV-IS-EG1) DNA was isolated from the infected *N. benthamiana*. The C1 ORF of TYLCV-IS-EG1 (SEQ ID 19 and 20) was produced as a 1.1-kb fragment by PCR amplification of infected plant DNA. The primers used were pTYIRc4 (SEQ ID 21) (5'-GGCCATAGAGCTTTGAGGGATCC CGATTCATTTC-3') and PTYC2v1679 (SEQ ID 22) (5'-GGTAGTAT GAGGATCCACAGTCTAGGTCT-3'). After BamHI-digesting the PCR products, they were ligated with BamHI-digested pBluescript II KS+ to produce pEGAL1-AS1, which contained the C1 ORF, as TYLCV-C1.

Example 4.2 **Synthesis of TYLCV-ΔC2*as***

A truncated C2 ORF (ΔC2) was produced as a 365 bp fragment by PCR amplification of TYLCV-IS-EG1-infected *N. benthamiana* DNA. The primers PTYC2v1499 (SEQ ID 32) (5'-ATTTGTGGATCCTGATTACCTTCCTGATGTTGTGG-3') and PTYC2c1814 (SEQ ID 35) (5'-AAACGGATCCTTGAAAAATTGGGC-3') were used. The primers were BamHI-digested and ligated into BamHI-digested pBluescript II KS+ to produce pTYC2-25-1, which contained the ΔC2 ORF in antisense orientation.

Example 4.3 **Synthesis of TYLCV-V1**

A truncated V1 ORF was produced as a 625-bp fragment by PCR amplification of TYLCV-IS-EG1 infected *N. benthamiana* DNA. The primers used were PTYAR1v466 (SEQ ID 33) (5'-TTAGGATCCTATATCTGTTGTAAGGGC-3') and PTYAR1c1046 (SEQ ID 34) (5'-TTAACTAATGCAGGATCCTACATTCCAGAGGGC-3').

The primers were BamHI-digested and ligated into BamHI-digested pBluescript II KS+ to produce pTYV1-6-1, which contains the V1 ORF.

Example 4.4 **Synthesis of TYLCV-C1-ΔC2-ΔC3**

A 1.3-kb fragment of the TYLCV-IS-EG1 genome from nt 1471 to nt 20 *via* nt 2787 (Navot *et al* 1991) was produced by PCR amplification of infected *N. benthamiana* DNA. The primers used were PTYIRc4 and PTYC2v1499. The primers were BamHI-digested and inserted into BamHI-digested pBluescript II KS+ to produce pTYEGC4.

Example 4.5 **Synthesis of TYLCV ORF Mutations**

A full-length infectious clone of TYLCV-IS-EG1 (pTYEG14) was created to serve as the basis for TYLCV ORF constructs and for agroinoculation (see below). DNA from a tomato infected with TYLCV-IS-EG1 was used as template in two PCR amplification reactions. The first used primers PTYC1c2196 (SEQ ID 37) (5'-AAATCTGCAGATGAACTAGAAGAGTGGG-3') and PTYV1v1164 (SEQ ID 36) (5'-GTACGAGAACCATACTGAAAACGCCT-3') to amplify a fragment. The PstI-SphI-digested fragment was ligated with PstI-SphI-digested pGEM-5zf+ (Promega) to produce plasmid pEGI1A.

The second amplification reaction employed primers PTYC1v2182 (SEQ ID 39) (5'-TAGGCCATGGCCGCGCAGCGGAATACACG-3') and PTYC3c1320 (SEQ ID 38) (5'-GGTTCTGCAGCAGAGCAGTTGATCATGTATTG-3'). The PstI-NcoI-digested fragment was ligated with PstI-NcoI-digested pGEM-5zf+ to produce pEGI1-7B.

To assemble the full-length virus, the PstI-NcoI fragment of pEGI1-7B was ligated with the PstI-NcoI fragment of pEGI1A to produce a construct comprising full-length 2.7-kb viral DNA. The full-length construct was tested for infectivity by biolistic delivery into tobacco cells and found to create

symptoms identical to the original disease. This clone was called pTYEG14. Orientation of insertion with respect to the f1 origin of replication was confirmed by DNA sequencing.

Three mutant C1 ORFs were constructed, each having one or two base changes altering the amino acid specificity of one codon by Kunkel mutagenesis using the plasmid representing the full-length infectious clone of TYLCV-IS-EG1 (pTYEG14) as template. The mutagenic primers (all viral sense) were:
PC1v2467 (SEQ ID 25) (5'-GTTTCCGTCTcgCTCCACGTAGG-3');
PC1v2101 (SEQ ID 28) (5'-GGCCCACATTGTTgCGCCTGTTCTGC-3'); and PC1v2000 (SEQ ID 31)
(5'-GGGTCTACGTCTctAATGACGTTGTACC-3'). (Lower case letters indicate altered nucleotides.) The resulting DNA was treated with T4 DNA ligase and transformed into XLI Blue *E. coli* cells to produce the following constructs: pTYK^{104}R #1 (SEQ ID 23 and 24), mutation 1(c); pTYK^{225}A #4 (SEQ ID 26 and 27), mutation 2(b); and pTYD^{259}R #5 (SEQ ID 29 and 30), mutation 3(a), described above.

The three mutant C1 ORFs were cloned into pCRII (Invitrogen). The C1 ORF for each mutant was PCR amplified using primers PTYIRc4 (SEQ ID 21) (5'-GGCCATAGAGCTTTGAGGATCCCGATTCATTTC-3') and PTYCv1707 (SEQ ID 42) (5'-GGTAGTATGAGGATCCACAGTCTAGGTCT-3'). The amplified fragments were ligated with pCRII to produce: pC1K^{104}R #2, mutation 1(c); pC1K^{225}A #4, mutation 2(b); and pC1D^{259}R #2, mutation 3(a), described above.

These three ORF in BamHI fragments of their respective vectors provided the mutant C1 ORFs for expression cassettes for *Agrobacterium* mediated transformation.

Example 5 **BGMV Constructions**

Wild-type and mutated versions of BGMV C1 (replication protein) ORF have been prepared. The wild-type sequence (SEQ ID 43 and 44) was mutated by Kunkel mutagenesis. Mutations in BGMV-C1 disclosed here include:

ORF	Mutant	SEQ ID	Mutagenic Primer
BGAC190	control	45	47
BGAC221	mutation 2(c)	48	50
BGAC228	mutation 2(a)	51	53
BGAC262	mutation 3(a)	54	56

SEQ ID NOS. 45, 48, 51, and 54, refer to mutagenized BGMV-C1 ORF DNA sequences presented in the Sequence Listing. These encode protein sequences 46, 49, 52, and 55, respectively. The mutant sequences were derived from wildtype DNA by Kunkel mutagenesis with mutagenic primers 47, 50, 53, and 56, respectively.

A 1.8Kb BamHI-XhoI fragment containing the 35S promoter transcriptionally fused to a mutated AC1 ORF from BGMV-GA followed by the nopaline synthase transcription terminator was removed from WRG2398 (Dr. D. R. Russell, Agracetus Corp., Middleton, WI). The AC1 coding sequence was mutated *in vitro* using Kunkel mutagenesis to produce double mutations 2(c) and 2(a). This fragment was ligated with pRT101e digested with the same enzymes and the ligation mix used to transform *E. coli* DH5 cells. Some transformants yielded desired recombinant plasmids that had the entire expression cassette from WRG2398 inserted into PRT101e (pJTS364). The new expression cassette was removed as a 2.9-Kb fragment from one of the recombinant plasmids by partial digestion with HindIII. It was ligated with pJTS246Δ that has been digested with HindIII and treated with CIAP. After transformation of DH5 cells, one recombinant among the transformants was identified that had the expression cassette inserted in the binary

vector. DNA of this binary vector was transformed into *A. tumefaciens* LBA4404 and one transformant containing the binary was called strain At^{364}.

Plasmid pJTS364 was digested with EcoRV to eliminate the duplicated 35S promoters (P_{35S}) and the cleaved DNA ligated. A fraction of the rejoined molecules have a deletion for the fragment between the *EcoRV* sites which contains the 35S enhancer (e_{35S}) from WRG2398 and P_{35S} from pRT101e. The ligation mix was used to transform DH5 cells. Among the transformants, the desired deleted plasmid was found and called pJTS365. The 2.5-Kb expression cassette was removed and ligated with HindIII-digested, CIAP treated pJTS246Δ. The ligation mix was used to transform DH5 cells. Recombinant binary plasmids were identified among the transformants and one of these was used as a source of DNA which was transformed into *A. tumefaciens* LBA4404. The transformed agrobacterium having the recombinant binary was called At^{365}.

The listed BGMV ORF are installed into appropriate promoter vectors and then into binary plasmids for *Agrobacterium*-mediated transformation into *Phaseolus* plants. Additionally, expression vectors are delivered into plants by biolistic acceleration or other methods by which plants can be transformed. Regenerated transformed plants are evaluated for levels of transgene RNA accumulation by RNA blot analysis to verify activity of the transgene. Subsequently, progeny are evaluated for ability to resist BGMV infection.

Example 6 **Expression Cassettes and *Agrobacterium* strains.**

The following ToMoV constructs were produced.

Example 6.1 **RTSC and RTAC**

The 1.1-kb BamHI fragment of pTFAC1, containing wild type AC1 ORF was inserted to the BamHI site of pRT101e. Antisense (pRTAC1-A) and sense (pRTAC1-S) constructs were produced. HindIII fragments of each plasmid were each inserted into the HindIII site of pJTS246Δ in the same transcriptional direction as the NPTII selectable marker. The binary vectors were transformed into LBA4404 to produce RTAC (antisense) and RTSC (sense).

Example 6.2 **DHSC and DHAC**

The wild type AC1 ORF was also inserted as a BamHI fragment into BamHI-digested pDH51 in both orientations creating pDHAC1-S (sense) and pDHAC1-AS (antisense). The expression cassette of each recombinant was removed with EcoRI and inserted into EcoRI-digested pJTS235. Recombinant binary plasmids were selected that had the expression cassette inserted such that the directions of transcription as the selectable marker. These binary plasmids were introduced into LBA4404 by transformation to produce DHSC (sense) and DHAC (antisense).

Example 6.3 **RTSFS**

pRTAC1-S was digested with BglII and flush ended by filling out. The resulting plasmid, pRTAC1-SΔBglII, lacked a BglII site but retained a core 4-base Sau3A site. This mutation shifted the translation reading frame by adding four nucleotides thereby producing a translation stop codon, and truncating the polypeptide (SEQ ID 13 and 14). A 2.1-kb HindIII fragment of pRTAC1-SΔBglII, which contains the expression cassette, was inserted in both orientations into the HindIII site of pJTS246Δ, unidirectional or divergent respecting the sense of selectable marker. A plasmid having an unidirectional orientation was introduced into LBA4404 by transformation to produce RTSFS.

Example 6.4 **RT3AA**

The 1.24-kb BglII-KpnI fragment of pSL1180+ΔAC1-AC2-AC3 was ligated into BglII-KpnI-digested pRTAC1-A to produce, pRT3AA, a pRT101e-like construct with the AC1, AC2 and AC3 ORFs inserted in antisense orientation. The 2.7 kb HindIII fragment of the pRT3AA was inserted into the HindIII site of pJTS246Δ in unidirectional orientation. The construct was introduced into LBA4404 by transformation to produce RT3AA.

Example 6.5 **LASD and LASU**

The 600-bp EcoRI-HincII fragment of pSL1180+PLAT52 was ligated with EcoRI-HincII-digested pRTAC1-S to replace the 800-bp 35S EcoRI-HincII promoter fragment by the 600-bp LAT52 EcoRI-HincII promoter fragment. After linearizing the plasmid with NcoI, the ATG start codon was destroyed by mung bean nuclease. The resulting plasmid contained an EcoRI and HindIII, but lacked a NcoI site. Accordingly, the sequences flanking the mutated NcoI site were the same as in the original LAT52 promoter untranslated 5' leader. The 5' untransformed leader was lengthened to 181 bp and included 68% A/T nucleotides. HindIII cut plasmid fragment containing the expression cassette was inserted into the HindIII site of pJTS246Δ in both unidirectional and divergent orientations respecting the sense of the selectable marker. One binary of each type was transformed into LBA4404 creating strains LASU and LASD, respectively.

Example 6.6 **MEU and MEU2**

The AC1 triple mutant (dlmAC1) ORF was removed as a 1.1-kb Xho I-BamHI fragment from its vector and inserted in the sense orientation into Xho I-Bam HI-digested pRT101e. A 2.1-kb expression cassette thus created was removed from pRT101e+AC1dlm by incompletely digesting the recombinant vector with HindIII and isolating a 2.1-kb fragment. This fragment was inserted into the HindIII site of pJTS246Δ to produce a

mutated enhanced unidirectional (MEU) vector. A second binary involving the same expression cassette which was tandemly duplicated in the unidirectional orientation was called MEU2. Both of the above binary vectors were transformed into LBA4404 to produce MEU and MEU2, respectively.

Example 6.7 **MUA and MUB**

ToMoV-AC1dlm1 was partially digested with HindIII and the 2.1-kb expression cassette was isolated. ToMoV-AC1dlm23 was completely digested with HindIII and the 2.1-kb cassette isolated. Each cassette was inserted into the HindIII site of pJTS246Δ. The recombinants were transformed into LBA4404 creating the *Agrobacterium* strains MUA and MUB, respectively.

Example 6.8 **MUAIN and MUBIN**

The 1.2 kb XhoI-BamHI-fragment of pRT101e+AC1 dlm1 containing the AC1dlm1 ORF was ligated with the XhoI-BamHI-fragment of pRTIN+Geneblock in a sense orientation. This construct was incompletely digested with HindIII followed by complete digestion with ScaI to produce a 2.6-kb fragment comprising the expression cassette. They were ligated with HindIII-digested pJTS246Δ in a divergent orientation respecting the selectable marker. The resulting *Agrobacterium* strain was called MUAIN.

The 2.1 kb BamHI fragment of pRT101e+ AC1dlm23, containing the AC1dlm23, was ligated with BamHI-digested OpRTIN+Geneblock plasmid in the sense orientation. This plasmid was digested with HindIII and ScaI producing a 2.6-kb expression cassette fragment which inserted into HindIII-digested pJTS246Δ in an unidirectional direction. Plasmid DNA from this clone was transformed into LBA4404 to produce MUBIN.

Example 6.9 **CODLM**

The 1.1 kb BamHI fragment containing the wild type AC1 ORF was inserted into the BamHI site of pΔ1CO35 in a sense orientation to produce pΔ1CO35+AC1S. The 4.5 kb ApaI-BglII fragment of pΔ1CO35+AC1S was restricted to delete a 475-bp comprising wild-type AC1 ORF and ligated to the ApaI-BglII fragment of pRT101e+AC1 dlm1 to replace the wild type internal fragment by the mutated fragment. The recombinant (pΔ1CO35+AC1 dlm) was incompletely digested with HindIII, the 2.4-kb fragment containing the expression cassette isolated and inserted into the HindIII site of pJTS246Δ in an unidirectional orientation. The plasmid was transformed into LBA4404 cells to produce CODLM.

Example 7 **Constructs Containing TYLCV-IS-EG1**

Example 7.1 **LCA**

The 1.1 kb BamHI fragment of pEGAL1-AS1 containing the C1 ORF was inserted in the BamHI site of pRT101e in an antisense orientation to produce pRTLCA1-A. A 2.1 kb HindIII fragment of pRTLCA1-A was inserted into the HindIII of pJTS246Δ in the unidirectional (U) orientation with regard to directions of transcription. LBA4404 cells were transformed with the resulting plasmid to produce LCA.

Example 7.2 **LCR'**

A 350-bp BamHI fragment encoding part of the C2 ORF of TYLCV-IS-EG1 was removed from pTYC2-25-1 and ligated into the BamHI site of pRT101e. The resulting construct contained the truncated C2 ORF inserted in an antisense orientation with respect to P_{35S}. The 1.3-kb expression cassette removed by HindIII digestion was inserted into the HindIII site of pJTS246Δ. Plasmid DNA of the resulting recombinant was partially digested with HindIII and ligated with the C1 antisense expression cassette. The desired plasmid had one copy of each the expression cassett inserted such that the

directions of transcription of all cassettes was unidirectional. DNA of this binary plasmid was transformed into LBA4404 to produce a strain, LCR', comprising the two-cassette recombinant binary plasmid.

Example 7.3 **LCR''**

A 620-bp BamHI fragment of pTYV1-6-1 encoding part of the V1 ORF of TYLCV-IS-EG1 was ligated into the BamHI site of pRT101e in an antisense orientation with respect to the 35S promoter. A HindIII fragment of the resulting plasmid was ligated into the HindIII site of pJTS246Δ in an unidirectional direction respecting the selectable marker. Plasmid DNA of this recombinant was transformed into LBA4404 to produce LCR''.

Example 7.4 **RT3CA**

The 1.3 kb BamHI fragment of pTYEGC4 containing the C1+ΔC2+ΔC3C structure was inserted into the BamHI site of pRT101e in an antisense manner with respect to the direction of transcription of the 35S promoter. The 2.3-kb HindIII fragment of pTYEGC4 the resulting plasmid containing the expression cassette was inserted into the HindIII site of pJTS246Δ in an unidirectional transcription directions. LBA4404 transformed with this plasmid to produce strain RT3CA.

The 1.3 kb BamHI fragment of pTYEGC4 comprising C1+ΔC2+ΔC3 DNA was ligated into the BamHI site of pΔ1Co35 in an antisense orientation with respect to the Commelina yellow mottle virus promoter. The 2.8 kb HindIII fragment of the resulting plasmid containing the expression cassette was inserted into the HindIII site of pJTS246Δ in an unidirectional orientation respecting the selectable marker. Plasmid DNA transformed into LBA4404 produced CO3CA.

The mutated 1.2 kb fragments containing C1 ORF were removed from their pCRII vectors and directionally ligated into the EcoRV-HindIII fragment of eP_{mas}-mcs-T_{phas}.

The resulting constructs were digested with XhoI and NaeI. HindIII fragments of pGA482Δ+HYG^R were flush ended by filling out, and digested with XhoI. The XhoI-NaeI expression cassettes were ligated into the binary vector that had an XhoI cohesive end and a blunt end to produce three constructs, C^{104}, C^{225} and C^{259}. DNA of each of the constructs were transformed into LBA4404 to produce the strains LC104, LC225 and LC259 and into *Agrobacterium* strain EHA105 (Mogen International, N.V.) to produce strains EC104, EC225 and EC259.

Example 7.5 **RT3CS**

The 1.3 kb BamHI fragment of pTYEGC4 containing the C1+ΔC2+ΔC3C structure was inserted into the BamHI site of pRT101e in an sense manner with respect to the direction of transcription of the 35S promoter. The 2.3-kb HindIII fragment of pTYEGC4 the resulting plasmid containing the expression cassette was inserted into the HindIII site of pJTS246Δ in an unidirectional transcription directions. LBA4404 transformed with this plasmid to produce strain RT3CS.

Example 8. **Production of Transgenic Plants Containing Disclosed Constructions and Analysis of Transgene Expression**

Transgenic plant were produced by *Agrobacterium*-co-cultivation procedures well known to those skilled in the art.

The media of compositions used are here defined, for 1 liter:

1/2X basal: 1/2X MS salts (Gibco), 10 g sucrose, 7 g agar, pH 5.8;

TCM: 1X MS salts, 30 g sucrose, 0.2 g KH_2PO_4, 1X N&N vitamins (Gibco), 0.1 mg 2,4-D, 0.05 mg kinetin, 20 mg acetosyringone, 7 g agar, pH 5.8

1Z: 1X MS salts, 30 g sucrose, 1X N&N vitamins, 1 mg zeatin, 100 mg kanamycine sulfate, 500 mg carbenicillin, 7 g agar, pH 5.8;

TR1: 1X MS salts, 30 g sucrose, 1X N&N vitamins, 3 mg glycine, 0.17 g NaH_2PO_4.H2O, 40 mg acetosyringone, pH 5.8;

MK5: 1/2X MS salts, 10 g sucrose, 1X N&N vitamins, 3 mg glycine, 0.17 g NaH_2PO_4.H2O, 50 mg kanamycin sulfate, 500 mg carbenicillin, 7 g agar, pH 5.8;

C: 1X MS salts, 30 g sucrose, 1X N&N vitamins, 3 mg glycine, 0.8 g NH_4NO_3, 2 mg BAP, 0.5 mg IAA, 100 mg kanamycine sulfate, 250 mg carbenicillin, 7g agar, pH 5.8.

Seeds were sterilized by briefly rinsing in 70% EtOH and then in a solution of 20% chlorox plus Tween-20. The seeds were dried in vacuo and then rinsed several times with sterile water. Washed seeds were transferred into 1/2X basal media and incubated in a Magenta box for about 7 days in 16 hour photoperiods daily.

Fully expanded cotyledons were cut aseptically under water. Two cuts were made at the end, and the tip of the cotyledon piece and the center piece was retained and used. A culture of *Agrobacterium* containing the appropriate binary plasmid was initiated 24 hours before co-cultivation. Bacteria in 4-5 ml of the culture were collected by centrifugation and resuspended in TR1-liquid media. The suspension was poured onto cut cotyledon pieces and incubated for about 25 min. The cotyledon pieces were placed on sterile filter papers and placed compactly on TCM medium. The plates were kept in the dark at room temperature for about 48 hours, after which they were placed on plates containing 1Z medium. The plates were incubated in 16 hours light daily at about 24° C for about 21 days.

Calli that formed on cotyledon pieces were transferred to fresh 1Z plates and shoots were removed as they

formed to 1/2-X MK-5 tubes for rooting. A 4-mm piece of leaf from the shoot was also placed on C medium for callus formation. Twelve to fourteen days after the plating on C medium, calli were scored as "-" or "+". About 60 to 70% of shoots with + callus root in MK5 media. Those that have + callus but did not root were trimmed off at the end and re-rooted on fresh MK5 tubes. About 80% of these will root on the second attempt.

Rooted shoots were removed to potting soil when a strong root system has developed, usually about 3 weeks after rooting. The plants were kept in a closed plastic bags for about 3 days, the bags were opened slowly after that to acclimatize the young plant. A 6- to 8-mm piece of leaf tissue was collected for the NPTII ELISA assay. The NPTII positive plants were transferred to the greenhouse for seed production. About 4 to 5 weeks in the greenhouse leaf tissues were collected for RNA isolation and Northern blots were done for these plants.

Example 9. **Analysis of Transgenic Plants**

Transgene RNA expression in transgenic tomato lines was accomplished by estimating steady state transcription levels using Northern blot hybridization. The level of transgene expression was used to select lines for agroinoculation. Total RNA was isolated from leaves and stems of young plants and electrophoresed on agarose gels.

The appropriate ORF DNA probe was radio-labeled and hybridized to RNA blotted on paper. After washing the RNA was visualized by autoradiography on X-ray film.

The following Tables 2, 3, and 4 summarize results showing plants produced with geminivirus constructs described above. The following symbols are used:

No+ or No-, Northern blot positive or negative;

So+ or So-, Southern blot positive or negative;

*, no data;

R_0 and R_1, primary and progeny lines.

Table 2 summarizes the transgenic tomato plants produced by transfer of wildtype ToMoV ORF DNA into the plant by Agrobacterium infection. For example, several tomato plants (TGM-1 to -17, -20, -24, -28, -29, -33 to -41, -47 to -49, -53, -54, -59 to -67, -70 to -131; TTGV92-1 to -5, -10, -13 to -20) were produced by Agrobacterium containing the RTAC construct. As shown in Table 1A, this construct is comprised of the ToMoV AC1 OFR in an antisense configuration. The predominant characteristic of these RTAC-containing plants is the presence of ToMoV DNA in the plant tissue (i.e., So+), transcribed RNA (i.e., No+), and transmitted these traits to their progeny (R_1 RNA). Table 2 also described transgenic plants with DHAC and RT3AA constructs, comprised of ToMoV AC1 and AC1-AC2-AC3 antisense ORF, respectively (Table 1A).

Table 3 describes transgenic tomato plant containing mutant ToMoV ORF. These include the meu, meu2, Codlm, mub, mua, mubin, mauin, rtsfs, lasu, and lasd constructs described in Table 1A.

Table 4 describes transgenic tomato plant containing TYLCV ORF. These include LCA, LCR, RT3CA, RT3CS and Co3CA constructs of Table 1A, comprising TYLCV C1, C2 and C3 ORF.

These results establish that the methods described herein produce transgenic plants using DNA constructs containing gemini virus ORF.

TABLE 2

TOMATO PLANTS TRANSFORMED WITH ToMoV

Product	Gene	R_0 RNA	R_1 RNA	R_0 DNA
Tgm-1, 10, 12, 14, 20, 29, 39, 53, 54, 64, 66, 70, 71, 80, 81, 82, 127	RTAC	No+	No+	So+
Tgm-3, 8, 13, 16, 17, 24, 28, 33, 34, 36, 40, 41, 47, 48, 49, 65, 114	RTAC	*	*	So+
Tgm-35	RTAC	*	*	So-
Tgm-59, 79, 102, 88, 116	RTAC	No-	No-	So+
Tgm-67	RTAC	No+	No-	So+
Tgm-84, 90, 93, 94, 97, 98, 99, 100, 101, 103, 106, 107, 108, 112, 113, 115, 117, 120, 121, 122, 123, 125, 129, 131	RTAC	No+	*	So+
Tgm-18, 19, 26, 42, 55, 58, 68	DHAC	*	*	So+
Tgm-23, 31, 44, 51	DHAC	No+	No+	So+
Tgm-27	DHAC	No-	No+	So+
3AA-3, 7, 9, 12, 13, 18, 21, 22, 23, 26, 27, 30	RT3AA	No+	*	*
3AA-4, 11, 16	RT3AA	No-	*	*
TTGV92-1	RTAC	No+	No-	So+
TTGV92-2, 5, 15, 17	RTAC	No-	*	So+
TTGV92-3, 13, 19	RTAC	No-	*	So-
TTGV92-4, 20	RTAC	No+	No+	So+
TTGV92-6, 20	DHAC	No+	No+	So+
TTGV92-7	DHAC	*	No+	So+
TTGV92-10	RTAC	No+	No+	*
TTGV92-11	DHAC	No+	*	So+
TTGV92-14	RTAC	No-	*	*
TTGV92-16	RTAC	*	*	So-

TABLE 3

TOMATO PLANTS TRANSFORMED WITH ToMoV REP ORF DOMINANT LETHAL MUTANT CONSTRUCTS

Product	Construct	R_0 RNA	R_1 RNA
TTGV92-26, 28, 36	meu2	*	*
TTGV92-27	meu2	No-	*
TTGV92-42	meu2	*	No+
DLM2, 39, 42, 46, 47, 48, 49, 51, 52, 55, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 79, 80, 81, 82, 83, 85, 88, 89, 90, 91, 93, 95, 96, 97, 98, 99, 100, 101, 102, 104, 106, 107, 108, 109, 110, 112, 116, 117, 118, 119, 120, 122, 124, 126, 127, 130, 133, 135, 136, 137, 139, 144, 148, 149, 151, 180, 155, 159, 162, 167, 170, 172, 173, 177, 192, 198, 200, 201, 204, 206, 211, 215, 217, 219, 220	meu	No+	*
DLM3, 5, 7, 9, 10, 12, 14, 15, 18, 21, 26, 30, 31	meu	No+	No+
DLM16	meu2	No-	No-
DLM17, 29	meu	*	*
DLM22	meu	No-	No-
DLM24	meu	No-	No-
DLM25	meu2	No+	No+
DLM27, 28	meu	No-	No-
DLM32	meu2	No+	No+
DLM37, 38, 44, 57, 59, 61, 75, 115, 129, 131, 138, 150, 166, 174, 179, 189, 208	meu	No-	*
DLM143	meu	No-	*
CODLM2, 4, 5, 6, 8, 9, 10, 13, 14, 15, 16, 18, 21, 24, 26, 28	Codlm	No+	*
CODLM3, 7, 19, 27	Codlm	No-	*
MU-2, 3, 4, 5, 6, 7, 14, 15, 19, 20, 26, 27, 30, 31, 32, 33, 34, 36, 37	mub	No+	*
MU-8, 9, 12, 16, 18, 22, 28, 39, 41	mua	No+	*
MU-11	mua	No-	*
MU-13, 47	mub	No-	*
MUIN-3, 6, 7	mubin	No+	*
MUIN-4, 5	muain	No+	*
MUIN-8, 10, 11, 14, 17, 18	mubin	*	*

Table 3, cont.

Product	Construct	R_0 RNA	R_1 RNA
MUIN-9, 15, 16, 19	muain	*	*
RTSFS-1, 3, 4, 6, 9, 10	rtsfs	No+	*
RTSFS-7, 8	rtsfs	No-	*
LAS-1	lasu	No+	*
LAS-6, 10	lasd	No+	*
LAS-11	lasd	No-	*

TABLE 4

TRANSGENIC TOMATO PLANTS TRANSFORMED WITH TYLCV GENE CONSTRUCTS

Product	Construct	R_0 DNA	R_0 RNA	R_1 RNA
Lca-1, 2, 37, 39, 43	lca	So-	*	*
Lca-5, 14, 21, 24, 29	lca	So+	*	No+
Lca-6, 35, 36, 46	lcr	So+	*	*
Lca-8, 12, 18, 19, 20, 26, 28	lca	So+	*	No-
Lca-25	lca	*	*	No-
Lca-45	lca	So+	No+	*
Lcr-1, 5, 6, 22	lcr	So+	No+	*
Lcr-3, 4, 17, 18, 20, 24	lcr	So-	No-	*
Lcr-12	lcr	So-	No+	*
Lcr-16, 31	lcr	So+	No-	*
Lcr-25	lcr	So+	*	*
Lcr-26, 27, 29, 32	lcr	So-	*	*
3CA-2, 3, -4, -6, -12, -15, -17, -18, -19, -21, -22	RT3CA	*	No+	*
CO3CA-1, -2, -4, -5, -7, -8, -9, -11, -12, -13, -14, -17, -18, -19	Co3CA	*	No+	*
CO3CA-6, -10	Co3CA	*	No-	*
RT3CS-1	RT3CS	*	No-	*

Example 10. Viral Challenge of Transgenic Plants

Example 10.1 ToMoV Agroinoculation Vector

A 5.6-kb fragment composed of a dimer of full-length infectious DNA-A was ligated with BamHI-HindIII digested binary plasmid pJTS222 to produce construct comprising the ToMoV-A dimer. The resulting plasmid produced transformed LBA4404 cells, uses as the A-component in agroinoculation experiments.

A 6.9-kb XbaI fragment that includes a full length infectious clone of DNA-B and the complete pBluescript II KS+ plasmid was inserted into the XbaI site of pJTS222. The resulting plasmid produced transformed LBA4404 cells used as the B-component in agroinoculation experiments.

Example 10.2 TYLC-IS-EG1 Agroinoculation Vector

The full length TYLCV-IS-EG1 DNA from infectious clone pTYEG14 was removed from the plasmid by SphI digestion and inserted at high molar excess into the SphI site of pGEM5Zf+ (Promega). The resulting plasmid, pTYEG7, contained a dimer of infectious TYLCV-IS-EG1 DNA. The 6.7-kb fragment of ScaI-PstI fragment of pTYEG7 comprised the dimer and part of pGEMZAf+. The 1.9-kb PstI-ScaI fragment of pSL1180 was ligated with the 6.7-kb fragment from pTYEG to produce a 8.7-kb construct with a single BglII site.

The 7.0 kb ScaI-BamHI fragment of the resulting recombinant plasmid was ligated with HpaI-BamHI-digested pJTS222. A resulting construct was used to transform LBA4404 c lls to produce AtLC1, which was used in the TYLCV agroinoculation experiments.

10.3 **Agroinoculation Procedure**

R_1 plants from self pollinated R_0 primary regenerants were agroinoculated 3 weeks after sowing. For bipartite geminiviruses, agroinoculation involves delivery of greater-than-full-length (must contain 2 common regions) ToMoV DNA-A and DNA-B into the seedlings using *Agrobacterium*. A small amount of a mixture of two *Agrobacterium* strains each containing a binary vector having in its T-DNA a partial or full tandem duplication of infectious geminivirus DNA was injected into the plant. For monopartite geminiviruses, only one agrobacterial strain is required if it carries a binary vector comprising a full or partial duplication of a full length infectious DNA.

Overnight cultures of *Agrobacteria* were diluted, and injected into stems of one month old tomato seedlings. About 100 hours later, a second inoculation identical to the first is performed.

Detection of NPTII by ELISA was taken as an indicium of the presence of the transgene. Agroinoculation experiments, summarized in Tables 5 to 10, show an array of resistance phenotypes. The data show several transgenic tomatoes resistant to ToMoV infection, including DLM12, TTGV92-42, CODLM6, CODLM8, CODLM13, CODLM14, MUA9, MUB20, MUA8, MUA18, MUA28, and MUA41.

Table 5. ToM V Agroinoculations - DLM Transgenics

Line (Generation)	Days Part Inoculation observation	Fraction of symptom-free and virus-free plants			
		NPTII positives		NPTII negatives	
		visual	blot	visual	blot
TTGV92-36 (R1)	20	2/16	2/16	0/2	0/2
TTGV92-42 (R1)	20	9/11	8/11	3/7	3/7
untransformed	20	*	*	0/17	0/17
DLM3 (R1)	26	*	5/16	*	0/2
DLM7 (R1)	26	*	4/15	*	1/3
DLM9 (R1)	26	*	0/14	*	1/2
DLM10 (R1)	26	*	2/16	*	0/2
DLM12 (R1)	26	*	10/17	*	0/1
untransformed	26	*	*	*	0/20
DLM12 (R1)	23	8/11	6/11	*	*
TTGV92-42-(R2)	23	*	*	3/18	2/18
TTGV92-42-(R2)	23	6/13	4/13	0/5	0/5
TTGV92-42 (R1)	23	13/15	10/15	0/3	0/3
untransformed	23	*	*	1/24	1/24
DLM12 (R1)	21	12/20	13/20	1/5	1/5
DLM14 (R1)	21	6/18	4/18	*	*
DLM15 (R1)	21	0/14	0/14	0/4	0/4
DLM27 (R1)	21	0/15	0/15	0/3	0/3
DLM28 (R1)	21	1/16	1/16	0/1	0/1
untransformed	21	*	*	0/15	0/15
DLM5 (R1)	18	0/13	1/13	0/5	0/5
DLM17 (R1)	18	1/5	1/5	3/9	3/9
DLM22 (R1)	18	0/15	0/15	0/3	0/3
DLM26 (R1)	18	2/3	2/3	1/5	1/5
DLM29 (R1)	18	0/13	0/13	1/3	1/3
DLM30 (R1)	18	3/14	3/14	1/4	1/4
DLM31 (R1)	18	4/12	4/12	0/6	0/6
TTGV92-42-17(R2)	18	7/13	6/13	1/4	1/4
TTGV92-42(R2)	18	17/18	17/18	*	*
untransformed	18	*	*	0/20	0/20
DLM16 (R1)	18	0/13	0/13	0/5	0/5
DLM18 (R1)	18	2/16	2/16	0/2	0/2

Table 5, cont.

Line (Generation)	Days Part Inoculation observation	Fraction of symptom-free and virus-free plants			
		NPTII positives		NPTII negatives	
		visual	blot	visual	blot
DLM21 (R1)	18	0/18	0/18	*	*
DLM24 (R1)	18	1/11	1/11	0/7	0/7
DLM25 (R1)	18	7/16	6/16	0/2	0/2
DLM32 (R1)	18	1/16	1/16	0/2	0/2
untransformed	18	*	*	0/13	0/13
DLM39 (R1)	30	0/15	1/15	1/4	1/4
DLM46 (R1)	18	0/15	0/15	0/5	0/5
DLM47 (R1)	18	5/17	4/17	0/3	0/3
DLM48 (R1)	18	0/15	0/15	0/5	0/5
DLM49 (R1)	18	1/16	9/16	0/4	0/4
DLM55 (R1)	18	0/14	0/14	0/6	0/6
DLM58 (R1)	18	0/14	1/14	0/6	0/6
untransformed	30	*	*	0/9	0/9

Table 6. ToMoV Agroinoculations: 3AA Transgenics

Line (Generation)	DPI observation	Fraction of symptom and virus free plants			
		NPTII positives		NPTII negatives	
		visual	blot	visual	blot
3AA3 (R1)	25	1/14	1/14	0/6	0/6
3AA7 (R1)	25	3/18	3/18	0/2	0/2
3AA9 (R1)	25	1/19	1/19	0/1	0/1
3AA12 (R1)	25	0/14	0/14	0/6	0/6
3AA13 (R1)	25	1/4	0/4	0/4	0/4
3AA16 (R1)	25	1/11	1/11	0/9	0/9
3AA18 (R1)	25	0/4	0/4	2/20	2/20
untransformed	25	*	*	0/15	0/15
3AA13 (R1)	22	2/19	2/19	0/1	0/1
3AA21 (R1)	25	3/13	3/13	0/7	0/7
3AA22 (R1)	22	6/16	9/16	0/4	0/4
3AA23 (R1)	25	3/9	4/9	0/1	0/1
3AA26 (R1)	25	0/16	0/16	0/4	0/4
3AA27 (R1)	25	0/10	0/10	0/4	0/4
3AA30 (R1)	25	2/18	5/18	0/2	0/2
untransformed	25	*	*	0/15	0/15

Table 7. ToMoV Agroinoculations: LAS Transgenics

Line (Generation)	DPI observation	Fraction of symptom and virus free plants			
		NPTII positives		NPTII negatives	
		visual	blot	visual	blot
LAS6 (R1)	25	8/11	8/11	0/9	0/9
LAS1 (R1)	25	0/10	0/10	0/10	0/10
LAS10 (R1)	25	1/14	1/14	1/6	1/6
LAS11 (R1)	25	*	*	0/20	0/20
untransformed	25	*	*	0/14	0/14

Table 8. ToM V Agroinoculati ns: CODLM Transg nics

Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants			
		NPTII positives		NPTII negatives	
		visual	blot	visual	blot
CODLM2 (R1)	20	0/14	0/14	0/6	0/6
CODLM5 (R1)	"	0/15	0/15	0/5	0/5
CODLM6 (R1)	"	9/14	3/14	0/6	0/6
CODLM8 (R1)	"	8/20	1/20	No NPTII-plants	"
CODLM9 (R1)	"	0/18	0/18	0/2	0/2
CODLM10 (R1)	"	0/17	0/17	0/3	0/3
CODLM13 (R1)	"	11/20	0/20	No NPTII-plants	"
CODLM14 (R1)	"	7/16	0/16	0/4	0/4
untransformed	"	"	"	1/9	1/9

Table 9. ToMoV Agroinoculations: MUA and MUB Transgenics

Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants			
		NPTII positives		NPTII negatives	
		visual	blot	visual	blot
MUA9	22	8/14	10/14	0/6	0/6
MUB20	"	10/20	1/20	No NPTII⁻	"
MUB37	"	1/14	0/14	0/6	0/6
MUB3	20	0/14	0/14	0/6	0/6
MUB5	"	1/7	0/17	0/3	0/3
MUB7	"	1/18	1/18	0/2	0/2
MUA8	"	6/6	5/6	0/14	0/14
MUA12	"	No NPTII⁺	"	0/20	0/20
MUB14	"	2/15	1/15	0/5	0/5
MUB15	"	5/20	3/20	No NPTII⁻	"
MUA16	"	5/14	4/14	0/6	0/6
MUA18	22	"	6/6	"	0/14
MUB19	"	"	1/11	"	No NPTII⁻
MUB26	"	"	0/15	"	0/5
MUA22	21	"	11/11	"	0/9
MUB33	"	"	0/15	"	0/5
MUB30	"	"	4/12	"	0/8
MUA28	"	"	12/12	"	0/7
MUA41	"	"	6/9	"	0/11
MUB36	"	"	1/15	"	0/5
MUA39	"	"	5/14	"	4/6
MUB31	"	"	2/16	"	0/4
MUB34	"	"	NO NPTII⁺	"	0/20
MUB32	"	"	3/16	"	0/4
untransformed	"	"	"	0/10	0/10

Tabl 10. ToM V Agroinoculations: RTFS Transg nics

Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants			
		NPTII positives		NPTII negatives	
		visual	blot	visual	blot
RTFS1	20	5/12	2/12	0/8	0/8
RTFS3	"	0/15	0/15	0/5	0/5
RTFS4	"	5/16	1/16	0/4	0/4
RTFS6	"	10/12	10/12	0/8	0/8
RTFS9	"	5/13	3/13	0/7	0/7
RTFS10	"	No NPTII*	"	0/20	0/20
untransformed	"	"	"	0/10	0/10

Example 10.4 **Squash Blot Assay of Geminivirus**

Approximately 3 weeks after agroinoculation, visible symptoms were monitored and compared to untransformed tomato lines. At the same time, two samples per plant of leaf extract were applied to a hybridization membrane. This was done by squashing a leaf disc about 1/8 inch diameter on the membrane such that leaf sap thoroughly impregnated the membrane. After the membrane was treated to denature the DNA in the extract, it was hybridized according to the same protocol as used for Northern blots with a radioactive probe that would detect the DNA-B component of ToMoV or the C1 ORF of TYLCV. The presence of viral DNA in the plant sap could be detected by autoradiography.

The presence of viral DNA was highly correlated with appearance of symptoms, an indicia of susceptibility to infection. The virus-free phenotype was correlated with the presence of the marker in families of transgenic tomatoes segregating the NPTII marker.

Figure 1 shows that expression of the ToMoV AC1dlm transgene is required for resistance to ToMoV infection

mediated by agroinoculation. High expression is necessary but in itself does not ensure resistance.

Example 10.4 **Viruliferous Whitefly Inoculations**

Ten whiteflies carrying ToMoV were put on each eight-day old seedling. Twenty-five seedlings were used per family. In those families of seedlings which were not homozygous for the transgene, NPTII assays were correlated with squash blot results. Twenty-one to thirty-one days after inoculation, samples of each plant were taken for biochemical and molecular hybridization assays. The results are summarized in Table 11. The Visual Rating gives the average of are plants, in which "0" is no symptoms and "4" is with most marked symptoms. The squash blot results give the fraction of the plants that were virus free.

Table 11. Florida Greenhouse Whitefly ToMoV Inoculations

Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants		Visual Ratings	Squash Blot Results
		NPTII Positives Blot	NPTII Negatives Blot		
		Blot	Blot		
TGM44 (R2)	21	7/20	0/6	2.2	13/26
TGM44 (R2)	21	6/17	0/9	1.6	10/26
untransformed	21	*	7/25	3.6	7/25
DLM12 (R2)	31	10/26	*	1.0	20/26
DLM12 (R2)	31	8/26	*	2.0	18/26
untransformed	31	*	1/19	3,7	3/19
DLM12 (R2)	31	8/20	*	0.8	8/20
DLM14 (R2)	31	3/11	*	1.7	3/11
DLM14 (R2)	31	9/23	*	3.0	12/23
untransformed	31	*	0/16	2.9	0/16
TTGV92-42 (R2)	32	7/21	1/5	2.5	23/26
TTGV92-42 (R3)	32	22/26	*	0	26/26
untransf.	32	*	*	3.8	6/15
XPH5978	32	*	10/26	2.9	No Data
XPH5979	32	*	7/26	2.7	No Data

Example 11. **Transdominance in plant cell lines**

A mutated form of AC1 protein of BGMV inhibits replication of DNA-A in a tobacco suspension cell system. To evaluate AC1 protein mutants for their potential to interfere with viral replication, a transient assay was used to detect trans-dominant interference activity of the mutant viral ORF. (Table 12 and Fig. 2.).

Table 12. Effects of BGMV AC1 Mutations on Replication and Transdominance

Mutation	Replication	Trans-dominance
WT AC1	+	0%
mutation 1(a)	-	90%
mutation 1(c)	-	90%
$I^{90}R$	+	0%
mutation 2(c)	+	0%*
mutation 2(a)	-	50-80%
mutation 3(a)	-	>95%
mutations 2(a) and (c)	-	50-80%

NT-1 cells were inoculated with wildtype DNA-A or a lethal mutant of DNA-A of BGMV-GA (ADM; double mutations 2(a) and (c) in combination with carrier DNA (PBS) or AC1 transexpression vectors containing mutated forms of AC1 ORF. Total DNA was harvested from the NT-1 tobacco cells at 72 hours after inoculation, electrophoresed in an agarose gel, blotted onto paper and probed with a radiolabeled DNA probe corresponding to the coat protein of BGMV-GA DNA-A. The results demonstrate that wildtype AC1 protein produced in trans can replicate a lethal AC1 mutant of DNA-A. More importantly, the results show that codon changes in the nicking motif of the AC1 ORF abolished infectivity and replication. In the transient assay for trans-dominance interference, double mutations 1(a) and 1(c) showed trans-dominance interference (Table 12).

Additional experimental treatments included:

A+PBS: wildtype BGMV-DNA-A was introduced into NT-1 cells with PBS at DNA weight ratios of 1:100 and 5:95 wildtype:PBS;

A+TDM: BGMV-DNA-A was introduced into NT-1 cells with transexpression vector coding for double mutations 2(a) and 2(c) at ratios of 1:100 and 5:95;

A+TD^{262}R: BGMV-DNA-A was introduced with transexpression vector coding for mutation 3(a) at ratios of 1:100 and 5:95;

ADM+PBS: DNA-A containing double mutations 2(a) and 2(c) with PBS at 5:95;

ADM+TAC1: DNA-A containing double mutations 2(a) and 2(c) with transexpression vector coding for wildtype AC1 at a ratio of 5:95.

The transexpression vectors used in these experiments express AC1 in the proper context for replication.

Figure 1 represents the results of these experiments. The mutations created in the 35S promoter driven AC1 ORF are listed in the first column. These ORF are used in trans with wild-type DNA-A of BGMV-GA to determine transdominance interference. Replication was tested in an NT-1 cell system. Replication is presented as the amount of reduction in replication in comparison to wild-type replication level. Trans-dominance was determined by engineering each mutation into a AC1 transexpression vectors which contained the AC1 ORF under control of the CaMV 35S promoter. Mutant AC1 expression vectors were coinoculated into NT-1 cells along with WT DNA-A and reductions in DNA-A replication were estimated from autoradiograms. Trans-dominance data are expressed as the observed reduction in DNA-A replication when co-inoculated with each AC1 mutant. Mutation 2(c) confers a temperature sensitive phenotype

for replication, supporting replication at 23°C but not at 28°C.

Replication was observed in inoculations with wildtype BGMV-DNA-A plus carrier DNA (A+PBS) (Fig. 1). No replication was observed in inoculations with a mutant of DNA-A containing double mutations 2(a) and 2(c) coinoculated with carrier DNA (ADM+PBS). Replication of double mutations 2(a) and 2(c) was, however, complemented by transexpression of wildtype AC1 in the transient expression vector (ADM+TAC1). Replication of BGMV-DNA-A in the presence of two different AC1 mutants, treatments A+TDM and A+TD^{262}R reduced replication of virus DNA-A compared to the A+PBS treatments. Accordingly, transexpression of AC1 mutants can inhibit replication of BGMV-DNA-A. Further lethal mutants of AC1 inhibit replication when expressed in trans to DNA-A.

The results show that non-lethal mutants do not exhibit detectable transdominant activity. While levels of transdominance varied among different AC1 mutants, only replication-lethal mutants exhibited transdominant interference. Levels of AC1 expression directly relate to levels of trans-dominance and replication (Fig. 1). Thus, AC1 expression, results in production of a protein that mediates the "trans"-effective suppression. That is, this protein likely binds to the CR region which mediates its suppressive effect by inhibiting the binding of the wildtype AC1 protein.

(1) GENERAL INFORMATION:

(i) APPLICANT: Stout, John T.
Luu, Hang T.
Maxwell, Douglas
Ahlquist, Paul
Hanson, Steve

(ii) TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus Genes

(iii) NUMBER OF SEQUENCES: 63

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
(B) STREET: 277 Park Avenue
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10172-0194

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING SYSTEM:
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Fitzpatrick, Cella, Harper, and Scinto

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-758-2400
(B) TELEFAX: 212-758-2982

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Gemini Virus
(C) INDIVIDUAL ISOLATE: Florida

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 44..1130

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Gilbertson, RL
Hidayat, SH
Paplomatas, EJ
Rojas, MR
Hou, YM
Maxwell, DP
(B) TITLE: Pseudorecombination between the infectious cloned DNA components of tomato mottle and bean dwarf mosaic geminiviruses.
(C) JOURNAL: Jour. General Virol.
(D) VOLUME: 74
(F) PAGES: 23-31
(G) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA        55
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Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln
  5                  10                  15                  20

TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT      151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn
                 25                  30                  35

ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA      199
Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg Glu Leu His Glu
             40                  45                  50

AAT GGG GAA CCT CAT CTC CAT GTG CTT GTT CAG TTC GAA GGA AAG TAC      247
Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe Glu Gly Lys Tyr
         55                  60                  65

CAG TGC ACG AAT AAC AGA TTC TTC GAC CTG GTC TCC CCA ACC CGG TCA      295
Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser Pro Thr Arg Ser
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GCA CAT TTC CAT CCG AAT ATT CAG GGA GCT AAA TCG AGC TCC GAC GTC      343
Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser Asp Val
 85                  90                  95                 100

AAA TCG TAC ATC GAC AAG GAC GGA GAT ACA ATC GAA TGG GGA GAT TTC      391
Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu Trp Gly Asp Phe
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CAG ATC GAC GGC AGA TCT GCC AGA GGA GGC CAG CAG TCT GCT AAT GAT      439
Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp
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        135                 140                 145

GTT CTA AGG GAA GAA CAA CCA AAA GAT TTT GTA TTA CAA AAT CAT AAC      535
Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu Gln Asn His Asn
    150                 155                 160

ATC CGC TCT AAC CTA GAA CGA ATA TTC GCA AAG GCT CCG GAA CCG TGG      583
Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala Pro Glu Pro Trp
165                 170                 175                 180

GTT CCT CCA TTT CAA GTC TCT TCT TTC ACT AAC GTT CCT GAC GAG ATG      631
Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val Pro Asp Glu Met
                185                 190                 195

CAG GAA TGG GCG GAT AAT TAT TTC GGG ACG GGT GCA GCT GCG CGG CCA      679
Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala Ala Ala Arg Pro
            200                 205                 210

GAG AGA CCT GTA AGT ATC ATC GTC GAG GGT GAT TCA AGA ACA GGG AAG      727
Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser Arg Thr Gly Lys
        215                 220                 225

ACG ATG TGG GCA CGT GCG TTA GGC CCA CAT AAC TAT CTC AGT GGA CAC      775
Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser Gly His
    230                 235                 240

CTA GAC TTC AAT GGT CGA GTC TTC TCG AAT GAT GTG CAG TAT AAC GTC      823
Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val Gln Tyr Asn Val
245                 250                 255                 260

ATT GAT GAC ATC GCA CCG CAT TAT CTA AAG CTA AAG CAC TGG AAA GAA      871
Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp Lys Glu
                265                 270                 275

TTG CTA GGG GCC CAG AAA GAT TGG CAA TCA AAT TGC AAG TAC GGT AAG      919
Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys Lys Tyr Gly Lys
            280                 285                 290

CCA GTT CAA ATT AAA GGC GGA ATC CCA GCA ATC GTG CTT TGC AAT CCT      967
Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val Leu Cys Asn Pro
        295                 300                 305

GGT GAG GGT GCC AGC TAT AAA GAG TTC TTA GAC AAA GCA GAA AAT ACA     1015
Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys Ala Glu Asn Thr
    310                 315                 320

GGT CTA AAG AAC TGG ACT GTC AAG AAT GCG ATC TTC ATC ACC CTC ACA     1063
Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe Ile Thr Leu Thr
325                 330                 335                 340

GCC CCC CTC TAT CAA GAC AGC ACA CAG GCA AGC CAA GAA ACG GGC AAT     1111
Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln Glu Thr Gly Asn
                345                 350                 355

CAG AAG GCG CAG GGT TGA T CTACAGTGCG GGTGCTCCAT CTACTTCCTA          1160
Gln Lys Ala Gln Gly  *
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363

GG 1162

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Pro Pro Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
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Gln Asn Leu Asn Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg
35 40 45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe
50 55 60

Glu Gly Lys Tyr Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser
65 70 75 80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
85 90 95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu
100 105 110

Trp Gly Asp Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
115 120 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln
130 135 140

Ser Ala Leu Ala Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu
145 150 155 160

Gln Asn His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala
165 170 175

Pro Glu Pro Trp Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val
180 185 190

Pro Asp Glu Met Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala
195 200 205

Ala Ala Arg Pro Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser
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Arg Thr Gly Lys T Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225 230 235 240

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Leu Ser Gly His Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val
                245                 250                 255

Gln Tyr Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys
            260                 265                 270

His Trp Lys Glu Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
        275                 280                 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val
    290                 295                 300

Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys
305                 310                 315                 320

Ala Glu Asn Thr Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe
                325                 330                 335

Ile Thr Leu Thr Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln
            340                 345                 350

Glu Thr Gly Asn Gln Lys Ala Gln Gly  *
        355                 360
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Gemini Virus
(B) STRAIN: Florida

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 44..1130

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Gilbertson, RL et al
(B) TITLE: Pseudorecombination between the infectious cloned DNA components of tomato mottle and bean dwarf mosaic geminivirus.
(C) JOURNAL: Journal of General Virology
(D) VOLUME: 74
(F) PAGES: 23-31
(G) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA

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                                                                  Met Pro Pro Pro
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Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln
            370                 375                 380

TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT      151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn
        385                 390                 395

ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA      199
Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg Glu Leu His Glu
    400                 405                 410

AAT GGG GAA CCT CAT CTC CAT GTG CTT GTT CAG TTC GAA GGA AAG TAC      247
Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe Glu Gly Lys Tyr
415                 420                 425                 430

CAG TGC ACG AAT AAC AGA TTC TTC GAC CTG GTC TCC CCA ACC CGG TCA      295
Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser Pro Thr Arg Ser
                435                 440                 445

GCA CAT TTC CAT CCG AAT ATT CAG GGA GCT AAA TCG AGC TCC GAC GTC      343
Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser Asp Val
            450                 455                 460

AAA TCG TAC ATC GAC AAG GAC GGA GAT ACA ATC GAA TGG GGA GAT TTC      391
Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu Trp Gly Asp Phe
        465                 470                 475

CAG ATC GAC GGC AGA TCT GCC AGA GGA GGC CAG CAG TCT GCT AAT GAT      439
Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp
    480                 485                 490

TCA TAT GCG AAA GCG TTA AAT GCA AGT TCG GTT CAA TCT GCC TTA GCA      487
Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln Ser Ala Leu Ala
495                 500                 505                 510

GTT CTA AGG GAA GAA CAA CCA AAA GAT TTT GTA TTA CAA AAT CAT AAC      535
Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu Gln Asn His Asn
                515                 520                 525

ATC CGC TCT AAC CTA GAA CGA ATA TTC GCA AAG GCT CCG GAA CCG TGG      583
Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala Pro Glu Pro Trp
            530                 535                 540

GTT CCT CCA TTT CAA GTC TCT TCT TTC ACT AAC GTT CCT GAC GAG ATG      631
Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val Pro Asp Glu Met
        545                 550                 555

CAG GAA TGG GCG GAT AAT TAT TTC GGG ACG GGT GCA GCT GCG CGG CCA      679
Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala Ala Ala Arg Pro
    560                 565                 570

GAG AGA CCT GTA AGT ATC ATC GTC GAG GGT GAT TCA AGA ACA GGG CAC      727
Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser Arg Thr Gly His
575                 580                 585                 590

ACG ATG TGG GCA CGT GCG TTA GGC CCA CAT AAC TAT CTC AGT GGA CAC      775
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                595                     600                 605

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Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val Gln Tyr Asn Val
            610                 615                 620

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Ile Lys Tyr Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp Lys Glu
        625                 630                 635

TTG CTA GGG GCC CAG AAA GAT TGG CAA TCA AAT TGC AAG TAC GGT AAG      919
Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys Lys Tyr Gly Lys
    640                 645                 650

CCA GTT CAA ATT AAA GGC GGA ATC CCA GCA ATC GTG CTT TGC AAT CCT      967
Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val Leu Cys Asn Pro
655                 660                 665                 670

GGT GAG GGT GCC AGC TAT AAA GAG TTC TTA GAC AAA GCA GAA AAT ACA     1015
Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys Ala Glu Asn Thr
                675                 680                 685

GGT CTA AAG AAC TGG ACT GTC AAG AAT GCG ATC TTC ATC ACC CTC ACA     1063
Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe Ile Thr Leu Thr
            690                 695                 700

GCC CCC CTC TAT CAA GAC AGC ACA CAG GCA AGC CAA GAA ACG GGC AAT     1111
Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln Glu Thr Gly Asn
        705                 710                 715

CAG AAG GCG CAG GGT TGA T CTACAGTGCG GGTGCTCCAT CTACTTCCAC          1160
Gln Lys Ala Gln Gly  *
    720

TTAGACTGT                                                          1169
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Gln Asn Leu Asn Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg
        35                  40                  45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe
    50                  55                  60
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Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85                  90                  95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu
            100                 105                 110

Trp Gly Asp Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
        115                 120                 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln
    130                 135                 140

Ser Ala Leu Ala Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu
145                 150                 155                 160

Gln Asn His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala
                165                 170                 175

Pro Glu Pro Trp Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val
            180                 185                 190

Pro Asp Glu Met Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala
        195                 200                 205

Ala Ala Arg Pro Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser
    210                 215                 220

Arg Thr Gly His Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225                 230                 235                 240

Leu Ser Gly His Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val
                245                 250                 255

Gln Tyr Asn Val Ile Lys Tyr Ile Ala Pro His Tyr Leu Lys Leu Lys
            260                 265                 270

His Trp Lys Glu Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
        275                 280                 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val
    290                 295                 300

Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys
305                 310                 315                 320

Ala Glu Asn Thr Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe
                325                 330                 335

Ile Thr Leu Thr Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln
            340                 345                 350

Glu Thr Gly Asn Gln Lys Ala Gln Gly *
        355                 360
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Gemini Virus
(B) STRAIN: Florida

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 44..1130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA          55
                                                Met Pro Pro Pro
                                                365

AAG AAA TTT AGA GTT CAG TCA AAG AAC TAT TTC CTC ACT TAT CCA CAG          103
Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln
            370                 375                 380

TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT          151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn
        385                 390                 395

ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA          199
Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg Glu Leu His Glu
    400                 405                 410

AAT GGG GAA CCT CAT CTC CAT GTG CTT GTT CAG TTC GAA GGA AAG TAC          247
Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe Glu Gly Lys Tyr
415                 420                 425                 430

CAG TGC ACG AAT AAC AGA TTC TTC GAC CTG GTC TCC CCA ACC CGG TCA          295
Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser Pro Thr Arg Ser
                435                 440                 445

GCA CAT TTC CAT CCG AAT ATT CAG GGA GCT AAA TCG AGC TCC GAC GTC          343
Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser Asp Val
            450                 455                 460

AAA TCG TAC ATC GAC AAG GAC GGA GAT ACA ATC GAA TGG GGA GAT TTC          391
Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu Trp Gly Asp Phe
        465                 470                 475

CAG ATC GAC GGC AGA TCT GCC AGA GGA GGC CAG CAG TCT GCT AAT GAT          439
Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp
    480                 485                 490

TCA TAT GCG AAA GCG TTA AAT GCA AGT TCG GTT CAA TCT GCC TTA GCA          487
```

```
Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln Ser Ala Leu Ala
495                 500                 505                 510

GTT CTA AGG GAA GAA CAA CCA AAA GAT TTT GTA TTA CAA AAT CAT AAC      535
Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu Gln Asn His Asn
                515                 520                 525

ATC CGC TCT AAC CTA GAA CGA ATA TTC GCA AAG GCT CCG GAA CCG TGG      583
Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala Pro Glu Pro Trp
            530                 535                 540

GTT CCT CCA TTT CAA GTC TCT TCT TTC ACT AAC GTT CCT GAC GAG ATG      631
Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val Pro Asp Glu Met
        545                 550                 555

CAG GAA TGG GCG GAT AAT TAT TTC GGG ACG GGT GCA GCT GCG CGG CCA      679
Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala Ala Ala Arg Pro
    560                 565                 570

GAG AGA CCT GTA AGT ATC ATC GTC GAG GGT GAT TCA AGA ACA GGG CAC      727
Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser Arg Thr Gly His
575                 580                 585                 590

ACG ATG TGG GCA CGT GCG TTA GGC CCA CAT AAC TAT CTC AGT GGA CAC      775
Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser Gly His
                595                 600                 605

CTA GAC TTC AAT GGT CGA GTC TTC TCG AAT GAT GTG CAG TAT AAC GTC      823
Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val Gln Tyr Asn Val
            610                 615                 620

ATT GAT GAC ATC GCA CCG CAT TAT CTA AAG CTA AAG CAC TGG AAA GAA      871
Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp Lys Glu
        625                 630                 635

TTG CTA GGG GCC CAG AAA GAT TGG CAA TCA AAT TGC AAG TAC GGT AAG      919
Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys Lys Tyr Gly Lys
    640                 645                 650

CCA GTT CAA ATT AAA GGC GGA ATC CCA GCA ATC GTG CTT TGC AAT CCT      967
Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val Leu Cys Asn Pro
655                 660                 665                 670

GGT GAG GGT GCC AGC TAT AAA GAG TTC TTA GAC AAA GCA GAA AAT ACA     1015
Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys Ala Glu Asn Thr
                675                 680                 685

GGT CTA AAG AAC TGG ACT GTC AAG AAT GCG ATC TTC ATC ACC CTC ACA     1063
Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe Ile Thr Leu Thr
            690                 695                 700

GCC CCC CTC TAT CAA GAC AGC ACA CAG GCA AGC CAA GAA ACG GGC AAT     1111
Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln Glu Thr Gly Asn
        705                 710                 715

CAG AAG GCG CAG GGT TGA T CTACAGTGCG GGTGCTCCAT CTACTTCCAC          1160
Gln Lys Ala Gln Gly  *
    720

TTAGACTGT                                                          1169
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Pro Pro Pro Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
 1               5                  10                  15

Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu
            20                  25                  30

Gln Asn Leu Asn Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg
        35                  40                  45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe
    50                  55                  60

Glu Gly Lys Tyr Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser
65                  70                  75                  80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85                  90                  95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu
            100                 105                 110

Trp Gly Asp Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
        115                 120                 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln
    130                 135                 140

Ser Ala Leu Ala Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu
145                 150                 155                 160

Gln Asn His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala
                165                 170                 175

Pro Glu Pro Trp Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val
            180                 185                 190

Pro Asp Glu Met Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala
        195                 200                 205

Ala Ala Arg Pro Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser
    210                 215                 220

Arg Thr Gly His Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225                 230                 235                 240

Leu Ser Gly His Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val
                245                 250                 255
```

```
Gln Tyr Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys
            250                 255                 270

His Trp Lys Glu Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
        275                 280                 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val
    290                 295                 300

Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys
305                 310                 315                 320

Ala Glu Asn Thr Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe
                325                 330                 335

Ile Thr Leu Thr Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln
            340                 345                 350

Glu Thr Gly Asn Gln Lys Ala Gln Gly  *
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Gemini Virus
(B) STRAIN: Florida

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 44..1130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA        55
                                                Met Pro Pro Pro
                                                365

AAG AAA TTT AGA GTT CAG TCA AAG AAC TAT TTC CTC ACT TAT CCA CAG      103
Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln
            370                 375                 380

TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT      151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn
        385                 390                 395

ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA      199
```

```
Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg Glu Leu His Glu
    400                 405                 410

AAT GGG GAA CCT CAT CTC CAT GTG CTT GTT CAG TTC GAA GGA AAG TAC      247
Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe Glu Gly Lys Tyr
415                 420                 425                 430

CAG TGC ACG AAT AAC AGA TTC TTC GAC CTG GTC TCC CCA ACC CGG TCA      295
Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser Pro Thr Arg Ser
                435                 440                 445

GCA CAT TTC CAT CCG AAT ATT CAG GGA GCT AAA TCG AGC TCC GAC GTC      343
Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser Asp Val
            450                 455                 460

AAA TCG TAC ATC GAC AAG GAC GGA GAT ACA ATC GAA TGG GGA GAT TTC      391
Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu Trp Gly Asp Phe
        465                 470                 475

CAG ATC GAC GGC AGA TCT GCC AGA GGA GGC CAG CAG TCT GCT AAT GAT      439
Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp
    480                 485                 490

TCA TAT GCG AAA GCG TTA AAT GCA AGT TCG GTT CAA TCT GCC TTA GCA      487
Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln Ser Ala Leu Ala
495                 500                 505                 510

GTT CTA AGG GAA GAA CAA CCA AAA GAT TTT GTA TTA CAA AAT CAT AAC      535
Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu Gln Asn His Asn
                515                 520                 525

ATC CGC TCT AAC CTA GAA CGA ATA TTC GCA AAG GCT CCG GAA CCG TGG      583
Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala Pro Glu Pro Trp
            530                 535                 540

GTT CCT CCA TTT CAA GTC TCT TCT TTC ACT AAC GTT CCT GAC GAG ATG      631
Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val Pro Asp Glu Met
        545                 550                 555

CAG GAA TGG GCG GAT AAT TAT TTC GGG ACG GGT GCA GCT GCG CGG CCA      679
Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala Ala Ala Arg Pro
    560                 565                 570

GAG AGA CCT GTA AGT ATC ATC GTC GAG GGT GAT TCA AGA ACA GGG AAG      727
Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser Arg Thr Gly Lys
575                 580                 585                 590

ACG ATG TGG GCA CGT GCG TTA GGC CCA CAT AAC TAT CTC AGT GGA CAC      775
Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser Gly His
                595                 600                 605

CTA GAC TTC AAT GGT CGA GTC TTC TCG AAT GAT GTG CAG TAT AAC GTC      823
Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val Gln Tyr Asn Val
            610                 615                 620

ATT AAA TAC ATC GCA CCG CAT TAT CTA AAG CTA AAG CAC TGG AAA GAA      871
Ile Lys Tyr Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp Lys Glu
        625                 630                 635

TTG CTA GGG GCC CAG AAA GAT TGG CAA TCA AAT TGC AAG TAC GGT AAG      919
```

```
Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys Lys Tyr Gly Lys
640                 645                 650

CCA GTT CAA ATT AAA GGC GGA ATC CCA GCA ATC GTG CTT TGC AAT CCT      967
Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val Leu Cys Asn Pro
655                 660                 665                 670

GGT GAG GGT GCC AGC TAT AAA GAG TTC TTA GAC AAA GCA GAA AAT ACA     1015
Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys Ala Glu Asn Thr
                675                 680                 685

GGT CTA AAG AAC TGG ACT GTC AAG AAT GCG ATC TTC ATC ACC CTC ACA     1063
Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe Ile Thr Leu Thr
            690                 695                 700

GCC CCC CTC TAT CAA GAC AGC ACA CAG GCA AGC CAA GAA ACG GGC AAT     1111
Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln Glu Thr Gly Asn
        705                 710                 715

CAG AAG GCG CAG GGT TGA T CTACAGTGCG GGTGCTCCAT CTACTTCCAC          1160
Gln Lys Ala Gln Gly  *
    720

TTAGACTGT                                                          1169
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Pro Pro Pro Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
 1               5                  10                  15

Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu
            20                  25                  30

Gln Asn Leu Asn Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg
        35                  40                  45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe
    50                  55                  60

Glu Gly Lys Tyr Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser
65                  70                  75                  80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85                  90                  95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu
            100                 105                 110

Trp Gly Asp Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
        115                 120                 125
```

```
Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln
    130                 135                 140

Ser Ala Leu Ala Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu
145                 150                 155                 160

Gln Asn His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala
                165                 170                 175

Pro Glu Pro Trp Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val
            180                 185                 190

Pro Asp Glu Met Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala
        195                 200                 205

Ala Ala Arg Pro Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser
    210                 215                 220

Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225                 230                 235                 240

Leu Ser Gly His Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val
                245                 250                 255

Gln Tyr Asn Val Ile Lys Tyr Ile Ala Pro His Tyr Leu Lys Leu Lys
            260                 265                 270

His Trp Lys Glu Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
        275                 280                 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val
    290                 295                 300

Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys
305                 310                 315                 320

Ala Glu Asn Thr Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe
                325                 330                 335

Ile Thr Leu Thr Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln
            340                 345                 350

Glu Thr Gly Asn Gln Lys Ala Gln Gly  *
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: FL25493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATCGGATCC GAGTAACTCA TCTGGAGTAC C 31

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: FL1108B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TATCGGATCC GGAAGTAGAT GGAGCACCCG C 31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PFAC1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAAGAACAGG GCACACGATG TGGG 24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PFAC1781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTATAACGTC ATTAAATACA TCGCACCGC 29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Geminivirus
(C) INDIVIDUAL ISOLATE: Florida

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 44..439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA        55
                                                Met Pro Pro Pro
                                                    365

AAG AAA TTT AGA GTT CAG TCA AAG AAC TAT TTC CTC ACT TAT CCA CAG       103
Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln
            370                 375                 380

TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT       151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn
        385                 390                 395

ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA       199
```

```
Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg Glu Leu His Glu
    400                 405                 410

AAT GGG GAA CCT CAT CTC CAT GTG CTT GTT CAG TTC GAA GGA AAG TAC      247
Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe Glu Gly Lys Tyr
415                 420                 425                 430

CAG TGC ACG AAT AAC AGA TTC TTC GAC CTG GTC TCC CCA ACC CGG TCA      295
Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser Pro Thr Arg Ser
                435                 440                 445

GCA CAT TTC CAT CCG AAT ATT CAG GGA GCT AAA TCG AGC TCC GAC GTC      343
Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser Asp Val
            450                 455                 460

AAA TCG TAC ATC GAC AAG GAC GGA GAT ACA ATC GAA TGG GGA GAT TTC      391
Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu Trp Gly Asp Phe
        465                 470                 475

CAG ATC GAC GGC AGA TCG ATC TGC CAG AGG AGG CCA GCA GTC TGC TAA      439
Gln Ile Asp Gly Arg Ser Ile Cys Gln Arg Arg Pro Ala Val Cys  *
    480                 485                 490

TGATTCATAT GCGAAAGCGT TAAATGCAAG TTCGGTTCAA TCTGCCTTAG CAGTTCTAAG    499

GGAAGAACAA CCAAAAGATT TTGTATTACA AAATCATAAC ATCCGCTCTA ACCTAGAACG    559

AATATTCGCA AAGGCTCCGG AACCGTGGGT TCCTCCATTT CAAGTCTCTT CTTTCACTAA    619

CGTTCCTGAC GAGATGCAGG AATGGGCGGA TAATTATTTC GGGACGGGTG CAGCTGCGCG    679

GCCAGAGAGA CCTGTAAGTA TCATCGTCGA GGGTGATTCA AGAACAGGGA AGACGATGTG    739

GGCACGTGCG TTAGGCCCAC ATAACTATCT CAGTGGACAC CTAGACTTCA ATGGTCGAGT    799

CTTCTCGAAT GATGTGCAGT ATAACGTCAT TGATGACATC GCACCGCATT ATCTAAAGCT    859

AAAGCACTGG AAAGAATTGC TAGGGGCCCA GAAAGATTGG CAATCAAATT GCAAGTACGG    919

TAAGCCAGTT CAAATTAAAG GCGGAATCCC AGCAATCGTG CTTTGCAATC CTGGTGAGGG    979

TGCCAGCTAT AAAGAGTTCT TAGACAAAGC AGAAAATACA GGTCTAAAGA ACTGGACTGT   1039

CAAGAATGCG ATCTTCATCA CCCTCACAGC CCCCCTCTAT CAAGACAGCA CACAGGCAAG   1099

CCAAGAAACG GGCAATCAGA AGGCGCAGGG TTGATCTACA GTGCGGGTGC TCCATCTACT   1159

TCCTAGG                                                             1166
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Pro Pro Pro Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
 1               5                  10                  15

Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu
            20                  25                  30

Gln Asn Leu Asn Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg
        35                  40                  45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe
    50                  55                  60

Glu Gly Lys Tyr Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser
65                  70                  75                  80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85                  90                  95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu
            100                 105                 110

Trp Gly Asp Phe Gln Ile Asp Gly Arg Ser Ile Cys Gln Arg Arg Pro
        115                 120                 125

Ala Val Cys  *
    130
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Geminivirus
(B) STRAIN: Florida

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Gilbertson, RL
Hidayat, SH
Paplomatas, EJ
Rojas, MR
Hou, YM
Maxwell, DP
(B) TITLE: Pseudorecombination between the infectious cloned DNA components of tomato mottle and bean dwarf mosaic geminiviruses.
(C) JOURNAL: Journal of General Virology
(D) VOLUME: 74
(F) PAGES: 23-31

(3) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGATCTGCCA GAGGAGGCCA GCAGTCTGCT AATGATTCAT ATGCGAAAGC GTTAAATGCA 60

AGTTCGGTTC AATCTGCCTT AGCAGTTCTA AGGGAAGAAC AACCAAAAGA TTTTGTATTA 120

CAAAATCATA ACATCCGCTC TAACCTAGAA CGAATATTCG CAAAGGCTCC GGAACCGTGG 180

GTTCCTCCAT TTCAAGTCTC TTCTTTCACT AACGTTCCTG ACGAGATGCA GGAATGGGCG 240

GATAATTATT TCGGGACGGG TGCAGCTGCG CGGCCAGAGA GACCTGTAAG TATCATCGTC 300

GAGGGTGATT CAAGAACAGG GAAGACGATG TGGGCACGTG CGTTAGGCCC ACATAACTAT 360

CTCAGTGGAC ACCTAGACTT CAATGGTCGA GTCTTCTCGA ATGATGTGCA GTATAACGTC 420

ATTGATGACA TCGCACCGCA TTATCTAAAG CTAAAGCACT GGAAAGAATT GCTAGGGGCC 480

CAGAAAGATT GGCAATCAAA TTGCAAGTAC GGTAAGCCAG TTCAAATTAA AGGCGGAATC 540

CCAGCAATCG TGCTTTGCAA TCCTGGTGAG GGTGCCAGCT ATAAAGAGTT CTTAGACAAA 600

GCAGAAAATA CAGGTCTAAA GAACTGGACT GTCAAGAATG CGATCTTCAT CACCCTCACA 660

GCCCCCCTCT ATCAAGACAG CACACAGGCA AGCCAAGAAA CGGGCAATCA GAAGGCGCAG 720

GGTTGATCTA CAGTGCGGGT GCTCCATCTA CTTCCACTTA GACTGTGCGG GACATGGATT 780

CACGCACAGG GGAACTCATC ACTGCACATC AGGCGGAGAA TGGCGTGTAT ATCTGGGAGC 840

TAAAAAATCC CCTTTATTTC AAGATACACA GGGTAGAGGA ACCACTGTAT ACCAGAACGA 900

GGGTATACCA CGTACAGATA CGGTTCAACC ACAACCTGAG GAAAGCGTTG CATCTCCACA 960

AAGCCTACCT GAACTTCCAA GTTTGGACGA CGTGGATGAC AGCTTCTGGA TCAATTTATT 1020

TAGCTAGATT TAGATATTTA GTCAACATGT ATCTAGATCA ATTAGGTGTT ATTTCAATAA 1080

ACAATGTAAT TAGAGCTGTA CGTTTCGCAA CAAACAGAGT GTATGTAAAT CATGTATTGG 1140

AGAATCATTC AATAAAATTC AAATTTTATT AATTCATGAT CGAATCATAA AAATAGATTC 1200

GAATTTTCAA AGTTGCATAT ACAGGGTTAG ACGCATGAGT GCATGC 1246

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

A. ORGANISM: FL-2549H

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TATCAAAGCT TGAGTAACTC ATCTGGAGTA CC 32

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Geminivirus
(B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGCATTTT TGTAATAAGA AGGGGTACTC CAGATGAGTT ACTCCAATTG AGCCTTCTCA 60

AACTTGCTCA TTCAATTGGA GTATTAGAGT AACTTATATA TAAGAACCCT CTATAGAACT 120

ATTAATCTGG TTCATACACG TGGCGGCCAT CCGATATAAT ATTACCGGAT GGCCGCGCGC 180

TTTTTTTTAA TCCGTACAGT CCAATACTCT CACATCCAAT CATAATGCGT CGTACAAGCC 240

TATATATTTC CAACAACTTG GGCCTTAAGT TGTTGGAGGC CCATTATAAA TTAAAGTGAT 300

CTTGGCCCAA TGTCTTTAAC TCAAAATGCC TAAGCGTGAT TTGCCATGGC GATCGATGGC 360

GGGAACCTCA AAGGTTAGCC GCAATGCTAA TTATTCTCCT CGTGCAGGTA TTAGGCCAAG 420

AATTAACAAG GCCGCTGAAT GGGTGAATCG GCCCATGTAT AGGAAGCCCA GGATCTATCG 480

GACTCTTAGT ACAACTGACG TGCCCAGGGG CTGTGAAGGC CCATGTAAGG TCCAGTCTTT 540

CGAACAGCGC CATGACATCT CACATATCGG TAAGGTCATG TGCATATCCG ATGTGACACG 600

TGGTAATGGC ATAACCCACC GTGTTGGTAA GCGTTTCTGT GTTAAGTCTG TGTATATCCT 660

TGGTAAGATT TGGATGGATG AGAACATCAA GCTCAAGAAC CACACGAATA GTGTCATGTT 720

CTGGTTGGTC AGAGATCGTA GACCCTATGG TACTCCAATG GATTTTGGAC AGGTGTTCAA 780

CATGTTCGAT AACGAGCCTA GCACTGCTAC TGTCAAAAAC GATCTACGCG ATCGTTACCA 840

GGTCATGCAT AAGTTCTATG GCAAGGTGAC AGGTGGACAG TATGCCAGCA ACGAGCAGGC 900

TATAGTTAAG AGGTTCTGGA AGGTGAACAA TCATGTAGTC TATAATCATC AAGAGGCTGG 960

CAAGTACGAG AATCACACAG AGAACGCCTT GTTATTGTAT ATGGCATGCA CTCATGCGTC 1920
TAACCCTGTA TATGCAACTT TGAAAATTCG AATCTATTTT TATGATTCGA TCATGAATTA 1980
ATAAAATTTG AATTTTATTG AATGATTCTC CAATACATGA TTTACATACA CTCTGTTTGT 2040
TGCGAAACGT ACAGCTCTAA TTACATTGTT TATTGAAATA ACACCTAATT GATCTAGATA 2100
CATGTTGACT AAATATCTAA ATCTAGCTAA ATAAATTGAT CCAGAAGCTG TCATCCACGT 2160
CGTCCAAACT TGGAAGTTCA GGTAGGCTTT GTGGAGATGC AACGCTTTCC TCAGGTTGTG 2220
GTTGAACCGT ATCTGTACGT GGTATACCCT CGTTCTGGTA TACAGTGGTT CCTCTACCCT 2280
GTGTATCTTG AAATAAAGGG GATTTTTTAG CTCCCAGATA TACACGCCAT TCTCCGCCTG 2340
ATGTGCAGTG ATGAGTTCCC CTGTGCGTGA ATCCATGTCC CGCACAGTCT AAGTGGAAGT 2400
AGATGGAGCA CCCGCACTGT AGATCAACCC TGCGCCTTCT GATTGCCCGT TTCTTGGCTT 2460
GCCTGTGTGC TGTCTTGATA GAGGGGGGCT GTGAGGGTGA TGAAGATCGC ATTCTTGACA 2520
GTCCAGTTCT TTAGACCTGT ATTTTCTGCT TTGTCTAAGA ACTCTTTATA GCTGGCACCC 2580
TCACCAGGAT TGCAAAGCAC GATTGCTGGG ATTCCGCCTT TAATTTGAAC TGGCTTACCG 2640
TACTTGCAAT TTGTTTGCCA ATCTTTCTGG GCCCCTAGCA ATTCTTTCCA GTGCTTTAGC 2700
TTTAGATAAT GCGGTGCGAT GTCATCAATG ACGTTATACT GCACATCATT CGAGAAGACT 2760
CGACCATTGA AGTCTAGGTG TCCACTGAGA TAGTTATGTG GGCCTAACGC ACGTGCCCAC 2820
ATCGTCTTCC CTGTTCTTGA ATCACCCTCG ACGATGATAC TTACAGGTCT CTCTGGCCGC 2880
GCAGCTGCAC CCGTCCCGAA ATAATTATCC GCCCATTCCT GCATCTCGTC AGGAACGTTA 2940
GTGAAAGAAG AGACTTGAAA TGGAGGAACC CACGGTTCCG GAGCCTTTGC GAATATTCGT 3000
TCTAGGTTAG AGCGGATGTT ATGATTTTGT AATACAAAAT CTTTTGGTTG TTCTTCCCTT 3060
AGAACTGCTA AGGCAGATTG AACCGAACTT GCATTTAACG CTTTCGCATA TGAATCATTA 3120
GCAGACTGCT GGCCTCCTCT GGCAGATCTG CCGTCGATCT GGAAATCTCC CCATTCGATT 3180
GTATCTCCGT CCTTGTCGAT GTACGATTTG ACGTCGGAGC TCGATTTAGC TCCCTGAATA 3240
TTCGGATGGA AATGTGCTGA CCGGGTTGGG GAGACCAGGT CGAAGAATCT GTTATTCGTG 3300
CACTGGTACT TTCCTTCGAA CTGAACAAGC ACATGGAGAT GAGGTTCCCC ATTTTCATGA 3360
AGCTCTCTGC AAATTTTGAT GAATTTCTTA TTGACTGGGG TATTTAGGTT TTGTAATTGG 3420
GAAAGTGCTT CTTCTTTAGA CAAAGAGCAC TGTGGATAAG TGAGGAAATA GTTCTTTGAC 3480
TGAACTCTAA ATTTCTTTGG TG 3502

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2540 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Mottle Geminivirus
(B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTGGCATTTT TGTAATAAGA AGGGGTACTC CAGATGAGTT ACTCCAATTG AGCCTTCTCA 60

AACTTGCTCA TTCAATTGGA GTATTAGAGT AACTTATATA TAAGAACCCT CTATAGAATT 120

ATTAATCTGG TTCATACACG TGGCGGCCAT CCGATATAAT ATTACCGGAT GGCCGCGCCC 180

CCCCCCCTTT TATACGCGCG CCTCTTTTGT CGTATTTCCA CGCTTCTTCC TGTTGGTGCG 240

TATCCTTCAC TTCCCATCTT TTTGAGTAGC CTTTAATTTG AATTAAAGGT TAAAACTTTA 300

TCGCGATGAC TAATCATATC ACATTGACCA TGTGAAGGAC GTGGCATTAT TTCGACCATG 360

CTGCTGAGTT TATTTGCTAT TATTGTTCTA TCCATAATCT ATATATTGGA TTGGTCAGGA 420

ATATTTTGTT TATCCAACTC AGCTGCATAC CACGTTTATA TCGTTAGCTA AATTTTGATT 480

AATCTTAGTT AAGTGTTTGA CTATGTATCC TTTAAAGTGT AAACGTGGTT TATCATATTC 540

AAATCGAAGA TTTAACTCAC GTAATAATGT GTTTAACCGT CCAGTTTCTG GTAAGAGACA 600

TGATGGAAAG CGTCGGGGAG GTAATTTCGT GAAGCCCAAT GATGAGCCCA AGATGTTAGC 660

CCAACGCATA CATGAGAATC AGTATGGGCC TGAATTTGTA TTGGCCCATA ACTCAGCTAT 720

CTCCACATTT ATCAGTTATC CCATCTTGGG CAAGTCCGAA GCCAGTCGAA GTAGGTCCTA 780

TATCAAGTTG AAACGTCTTC GTTTCAAAGG GACTGTGAAG ATTGAGCGTG TTCAATCTGA 840

TTTGAACATG GATGGCTTTA TGCCTAAAGT CGAAGGAGTA TTCTCTATGG TTGTTGTTGT 900

GGATCGTAAA CCACACTTGG GTCCCTCCGG GTGTTTGCAT ACATTCGACG AGCTATTTGG 960

TGCAAGGATC AATAGTCATG GCAACCTCAC TATAGTACCT TCTCTGAAAG ACCGCTTCTA 1020

CATTAGACAT GTGTTCAAGC GAGTGCTCTC AGTTGAGAAG GATACGTTGA TGGTGGACGT 1080

TGAAGGATCC ACAACACTCT CTAACAGGCG TTACAACTGC TGGTCTACGT TTAAAGACCT 1140

TGATCGTGAA TCATGCAAGG GTGTTTATGA TAACATTAGC AAGAACGCCT TGTTAGTTTA 1200

TTATTGCTGG ATGTCTGACA CGCCTTCGAA TGCATCCTCT TTTGTATCTT TTGATCTTGA 1260

TTATATTGGT TAACTTAACG AAGTGTGTTT GTCTAAAGAT GATTAAAAAA ATGAAAATGT 1320

AAAAATAAAA TTTTATTTTA ATGGTTTCGT GTGAGACGCC TTACAATTAC TATTAATACA 1380
TTCATGGACC GTAGTCCGTA TTAATTCATT CAACTGTCCC ATAGACATTG TAATGTTGGA 1440
CTCTGTTCTC TGGGCCCCCA CAATAGAAGC AGACTCTCCC GGGTCCAGTA TGCCTGTTCC 1500
TAGCCTGTTT AGATGTCTGT ACGGGTGGAG TTCGTTCTCC ACATCTGAGT CCGCATCTGA 1560
ATGCCCTATG CCTATTGTAC TCCTTGAAGC CCATGACTCA CCAGGCCTGA TCTCAATTGG 1620
ACCTCTAAGC CCAAGTCTGG ACATGGACGC GCATCTAATG GGCTTCCTCT CCCATTTACC 1680
GTAATCCACA TGGGAAAAGT CCACATCTTT ATCTGTGAAC TGTTTGGACA GGATTTTTAC 1740
TGTTGGTGCC CGGAAGGGGA TGTCTACTGA GTGTTTTGCT GTGGACAATT TCAGCTTCCC 1800
CTTAAACTTG GCGAAGTGGG TCCGTTGATG AACATTCGTA TCGCAAACCC TGTAATACAA 1860
TTTCCATGGA ATTGGGTCTT TCAAGGAGAA GAAGGAAGCT GAGAAATAGT GGAGATCTAT 1920
GTTGCACCTG ATCGGAAATG TCCATGATGC CTGTAAAGAC TCATTCTCCG TCATTCTTTT 1980
GTCGTGAATC TCCACTATTA CCGACCCAGT GGCGTTTATT GGTACTTGTT GTCTGTACTC 2040
TATGACACAG TGGTCGATTT TCATGCAGCT ACGGCTGAGC CTAGCGGTTA ACTGCGACGC 2100
CGTGGACGGA AATTGCAGTA TTATTTCAGT TAGGTCATGA GAAAGCTGAT ATTCGTCACG 2160
GTGTGCATCT ATGTAGTTGA ATGCGCTAGG AGGATTAACT AACTGAGAAT CCATATGAAG 2220
AAAATAAGGC CGCGCAGGAC TGATTGCTGA AGTTGAATCA GAAAGAAGTC GAACAAGCTA 2280
TGAAACGGCA GTTTCGAACT CGAAGAAGAA AGACAGCCAA CTATATTTTC TTTTTTCCAA 2340
GAATTCAGCT GTGCTGAATA TAAAGTTTAT GAAGAGCGGA AATGAAAAAA AGTATATCAG 2400
GATTCGAAGT GTTTGAGAAA GAAAAGAAAT ATGAAAGAGA ATTTTGGAGA AATTTGAGTA 2460
AGAAGGAATT TGTATATGAA CTAAGAAACC TAGGGTTGAT GGGTATTTAA ATTGGTAAAG 2520
TGTTCATCCC ATGAGATAGA 2540

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Yellow Leaf Curl Virus

S STRAIN: Israel

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 37..1110

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Navot, N
Pichersky, R
Zeidan, D
Zamir, D
Czosnek, H
(B) TITLE: Tomato yellow leaf curl virus: A whitefly-transmitted geminivirus with a single genomic component.
(C) JOURNAL: Virology
(D) VOLUME: 185
(F) PAGES: 151-168
(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC ATG CCT CGT TTA TTT AAA          54
                                        Met Pro Arg Leu Phe Lys
                                            135

ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAT TGT TCT CTC TCT          102
Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser
    140                 145                 150

AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT          150
Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn
155                 160                 165                 170

AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA          198
Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro
                175                 180                 185

CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC          246
His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn
            190                 195                 200

CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT          294
Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His
        205                 210                 215

CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG          342
Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val
    220                 225                 230

GAG AAA GAC GGA AAC TTC ATT GAT TTT GGA GTT TCC CAA ATC GAT GGC          390
Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly
235                 240                 245                 250

AGA TCA GCT AGA GGA GGT CAG CAA TCT GCC AAC GAC GCA TAT GCC GAA          438
Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp Ala Tyr Ala Glu
                255                 260                 265

GCA CTC AAT TCA GGC AGT ATA TCC GAG GCC CTC AAT ATA TTA AAA GAG          486
Ala Leu Asn Ser Gly Ser Ile Ser Glu Ala Leu Asn Ile Leu Lys Glu
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                270                 275                 280

AAG GCC CCA AAG GAC TAT ATT TTA CAA TTT CAT AAT TTA AGT TCA AAT
Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe His Asn Leu Ser Ser Asn
        285                 290                 295

TTA GAT AGG ATT TTT AGT CCT CCT TTA GAA GTT TAT GTT TCT CCA TTT
Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu Val Tyr Val Ser Pro Phe
    300                 305                 310

CTT TCT TCT TCT TTT AAT CAA GTT CCA GAT GAA CTT GAA GAG TGG GTC
Leu Ser Ser Ser Phe Asn Gln Val Pro Asp Glu Leu Glu Glu Trp Val
315                 320                 325                 330

GCC GAG AAC GTC GTG TAT TCC GCT GCG CGG CCA TGG AGA CCC ATA AGT
Ala Glu Asn Val Val Tyr Ser Ala Ala Arg Pro Trp Arg Pro Ile Ser
                335                 340                 345

ATT GTC ATT GAG GGT GAT AGC AGA ACA GGC AAA ACA ATG TGG GCC AGG
Ile Val Ile Glu Gly Asp Ser Arg Thr Gly Lys Thr Met Trp Ala Arg
            350                 355                 360

TCT CTA GGC CCA CAT AAT TAT TTA TGT GGA CAT CTA GAC CTA AGC CCA
Ser Leu Gly Pro His Asn Tyr Leu Cys Gly His Leu Asp Leu Ser Pro
        365                 370                 375

AAG GTG TAC AGT AAT GAT GCG TGG TAC AAC GTC ATT GAT GAC GTA AAC
Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn Val Ile Asp Asp Val Asn
    380                 385                 390

CCG CAT TAT TTA AAG CAC TTC AAG GAA TTC ATT TGG GCC CAG AGG GAC
Pro His Tyr Leu Lys His Phe Lys Glu Phe Ile Trp Ala Gln Arg Asp
395                 400                 405                 410

TGG CAA AGC AAC ACA AAG TAC GGG AAG CCC ATT CAA ATT AAA GGG GGA
Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro Ile Gln Ile Lys Gly Gly
                415                 420                 425

ATT CCC ACT ATC TTC CTC TGC AAT CCA GGA CCT ACC TCC TCA TAT AGG
Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly Pro Thr Ser Ser Tyr Arg
            430                 435                 440

GAA TAT CTA GAC GAA GAA AAA AAC ATA TCC TTG AAA AAT TGG GCT CTC
Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser Leu Lys Asn Trp Ala Leu
        445                 450                 455

AAG AAT GCA ACC TTC GTC ACC CTC TAC GAG CCA CTG TTC GCA AGT ATC
Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu Pro Leu Phe Ala Ser Ile
    460                 465                 470

AAT CAA GGT CCA ACA CAA GAT AGC CAA GAA GAA ACC AAT AAG GCG TAA
Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu Glu Thr Asn Lys Ala  *
475                 480                 485                 490

GCGTGTAGAC CTAGACTGTG GCTGCTCATA CTACC
```

1110 1145

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Pro Arg Leu Phe Lys Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr
1 5 10 15

Pro Asn Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys
20 25 30

Leu Glu Thr Pro Thr Asn Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu
35 40 45

His Glu Asn Gly Glu Pro His Leu His Val Leu Ile Gln Phe Glu Gly
50 55 60

Lys Tyr Gln Cys Lys Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Asn
65 70 75 80

Arg Ser Ala His Phe His Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr
85 90 95

Asp Val Lys Thr Tyr Val Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly
100 105 110

Val Ser Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala
115 120 125

Asn Asp Ala Tyr Ala Glu Ala Leu Asn Ser Gly Ser Ile Ser Glu Ala
130 135 140

Leu Asn Ile Leu Lys Glu Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe
145 150 155 160

His Asn Leu Ser Ser Asn Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu
165 170 175

Val Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asn Gln Val Pro Asp
180 185 190

Glu Leu Glu Glu Trp Val Ala Glu Asn Val Val Tyr Ser Ala Ala Arg
195 200 205

Pro Trp Arg Pro Ile Ser Ile Val Ile Glu Gly Asp Ser Arg Thr Gly
210 215 220

Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn Tyr Leu Cys Gly
225 230 235 240

His Leu Asp Leu Ser Pro Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn
245 250 255

Val Ile Asp Asp Val Asn Pro His Tyr Leu Lys His Phe Lys Glu Phe
260 265 270

Ile Trp Ala Gln Arg Asp Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro

275 280 285

Ile Gln Ile Lys Gly Gly Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly
290 295 300

Pro Thr Ser Ser Tyr Arg Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser
305 310 315 320

Leu Lys Asn Trp Ala Leu Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu
325 330 335

Pro Leu Phe Ala Ser Ile Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu
340 345 350

Glu Thr Asn Lys Ala *
355

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PTYIRC4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTC 33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PTYC1V[redacted]
1679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTAGTATGA GGATCCACAG TCTAGGTCTA CACGCTTAC 39

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Yellow Leaf Curl Geminivirus
(B) STRAIN: Israel

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 37..1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC ATG CCT CGT TTA TTT AAA          54
                                        Met Pro Arg Leu Phe Lys
                                            360

ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAT TGT TCT CTC TCT          102
Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser
365                 370                 375                 380

AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT          150
Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn
                385                 390                 395

AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA          198
Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro
            400                 405                 410

CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC          246
His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn
        415                 420                 425

CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT          294
Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His
    430                 435                 440

CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG          342
Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val
445                 450                 455                 460

GAG CGA GAC GGA AAC TTC ATT GAT TTT GGA GTT TCC CAA ATC GAT GGC          390
Glu Arg Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly
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                    465                 470                 475

AGA TCA GCT AGA GGA GGT CAG CAA TCT GCC AAC GAC GCA TAT GCC GAA
Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp Ala Tyr Ala Glu      438
            480                 485                 490

GCA CTC AAT TCA GGC AGT AAA TCC GAG GCC CTC AAT ATA TTA AAA GAG
Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala Leu Asn Ile Leu Lys Glu      486
        495                 500                 505

AAG GCC CCA AAG GAC TAT ATT TTA CAA TTT CAT AAT TTA AGT TCA AAT
Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe His Asn Leu Ser Ser Asn      534
    510                 515                 520

TTA GAT AGG ATT TTT AGT CCT CCT TTA GAA GTT TAT GTT TCT CCA TTT
Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu Val Tyr Val Ser Pro Phe      582
525                 530                 535                 540

CTT TCT TCT TCT TTT AAT CAA GTT CCA GAT GAA CTT GAA GAG TGG GTC
Leu Ser Ser Ser Phe Asn Gln Val Pro Asp Glu Leu Glu Glu Trp Val      630
                545                 550                 555

GCC GAG AAC GTC GTG TAT TCC GCT GCG CGG CCA TGG AGA CCC ATA AGT
Ala Glu Asn Val Val Tyr Ser Ala Ala Arg Pro Trp Arg Pro Ile Ser      678
            560                 565                 570

ATT GTC ATT GAG GGT GAT AGC AGA ACA GGC AAA ACA ATG TGG GCC AGG
Ile Val Ile Glu Gly Asp Ser Arg Thr Gly Lys Thr Met Trp Ala Arg      726
        575                 580                 585

TCT CTA GGC CCA CAT AAT TAT TTA TGT GGA CAT CTA GAC CTA AGC CCA
Ser Leu Gly Pro His Asn Tyr Leu Cys Gly His Leu Asp Leu Ser Pro      774
    590                 595                 600

AAG GTG TAC AGT AAT GAT GCG TGG TAC AAC GTC ATT GAT GAC GTA GAC
Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn Val Ile Asp Asp Val Asp      822
605                 610                 615                 620

CCG CAT TAT TTA AAG CAC TTC AAG GAA TTC ATG GGG GCC CAG AGG GAC
Pro His Tyr Leu Lys His Phe Lys Glu Phe Met Gly Ala Gln Arg Asp      870
                625                 630                 635

TGG CAA AGC AAC ACA AAG TAC GGG AAG CCC ATT CAA ATT AAA GGG GGA
Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro Ile Gln Ile Lys Gly Gly      918
            640                 645                 650

ATT CCC ACT ATC TTC CTC TGC AAT CCA GGA CCT ACC TCC TCA TAT AGG
Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly Pro Thr Ser Ser Tyr Arg      966
        655                 660                 665

GAA TAT CTA GAC GAA GAA AAA AAC ATA TCC TTG AAA AAT TGG GCT CTC
Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser Leu Lys Asn Trp Ala Leu     1014
    670                 675                 680

AAG AAT GCA ACC TTC GTC ACC CTC TAC GAG CCA CTG TTC GCA AGT ATC
Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu Pro Leu Phe Ala Ser Ile     1062
685                 690                 695                 700

AAT CAA GGT CCA ACA CAA GAT AGC CAA GAA GAA ACC AAT AAG GCG TAA
Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu Glu Thr Asn Lys Ala  *       1110
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705 710 715

GCGTGTAGAC CTAGACTGTG GCTGCTCATA CTACC 1145

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Pro Arg Leu Phe Lys Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr
1 5 10 15

Pro Asn Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys
20 25 30

Leu Glu Thr Pro Thr Asn Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu
35 40 45

His Glu Asn Gly Glu Pro His Leu His Val Leu Ile Gln Phe Glu Gly
50 55 60

Lys Tyr Gln Cys Lys Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Asn
65 70 75 80

Arg Ser Ala His Phe His Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr
85 90 95

Asp Val Lys Thr Tyr Val Glu Arg Asp Gly Asn Phe Ile Asp Phe Gly
100 105 110

Val Ser Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala
115 120 125

Asn Asp Ala Tyr Ala Glu Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala
130 135 140

Leu Asn Ile Leu Lys Glu Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe
145 150 155 160

His Asn Leu Ser Ser Asn Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu
165 170 175

Val Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asn Gln Val Pro Asp
180 185 190

Glu Leu Glu Glu Trp Val Ala Glu Asn Val Val Tyr Ser Ala Ala Arg
195 200 205

Pro Trp Arg Pro Ile Ser Ile Val Ile Glu Gly Asp Ser Arg Thr Gly
210 215 220

Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn Tyr Leu Cys Gly
225 230 235 240

His Leu Asp Leu Ser Pro Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn
245 250 255

Val Ile Asp Asp Val Asp Pro His Tyr Leu Lys His Phe Lys Glu Phe
260 265 270

Met Gly Ala Gln Arg Asp Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro
275 280 285

Ile Gln Ile Lys Gly Gly Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly
290 295 300

Pro Thr Ser Ser Tyr Arg Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser
305 310 315 320

Leu Lys Asn Trp Ala Leu Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu
325 330 335

Pro Leu Phe Ala Ser Ile Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu
340 345 350

Glu Thr Asn Lys Ala *
355

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: C1V2467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTTTCCGTCT CGCTCCACGT AGG 23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Yellow Leaf Curl Virus
(B) STRAIN: Israel

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 37..1110

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Navot, N
Pichersky, R
Zeidan, D
Zamir, D
Czosnek, H
(B) TITLE: Tomato yellow leaf curl virus: A whitefly-transmitted geminivirus with a single genomic component.
(C) JOURNAL: Virology
(D) VOLUME: 185
(F) PAGES: 151-168
(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC ATG CCT CGT TTA TTT AAA          54
                                        Met Pro Arg Leu Phe Lys
                                            360

ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAC TGT TCT CTC TCT          102
Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser
365                 370                 375                 380

AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT          150
Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn
                385                 390                 395

AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA          198
Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro
            400                 405                 410

CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC          246
His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn
        415                 420                 425

CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT          294
Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His
    430                 435                 440

CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG          342
Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val
445                 450                 455                 460

GAG AAA GAC GGA AAC TTC ATT GAT TTT GGA GTT TCC CAA ATC GAT GGC          390
Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly
                465                 470                 475
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AGA TCA GCT AGA GGA GGT CAG CAA TCT GCC AAC GAC GCA TAT GCC GAA                 438
Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp Ala Tyr Ala Glu
                480                 485                 490

GCA CTC AAT TCA GGC AGT AAA TCC GAG GCC CTC AAT ATA TTA AAA GAG                 486
Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala Leu Asn Ile Leu Lys Glu
        495                 500                 505

AAG GCC CCA AAG GAC TAT ATT TTA CAA TTT CAT AAT TTA AGT TCA AAT                 534
Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe His Asn Leu Ser Ser Asn
    510                 515                 520

TTA GAT AGG ATT TTT AGT CCT CCT TTA GAA GTT TAT GTT TCT CCA TTT                 582
Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu Val Tyr Val Ser Pro Phe
525                 530                 535                 540

CTT TCT TCT TCT TTT AAT CAA GTT CCA GAT GAA CTT GAA GAG TGG GTC                 630
Leu Ser Ser Ser Phe Asn Gln Val Pro Asp Glu Leu Glu Glu Trp Val
                545                 550                 555

GCC GAG AAC GTC GTG TAT TCC GCT GCG CGG CCA TGG AGA CCC ATA AGT                 678
Ala Glu Asn Val Val Tyr Ser Ala Ala Arg Pro Trp Arg Pro Ile Ser
            560                 565                 570

ATT GTC ATT GAG GGT GAT AGC AGA ACA GGC GCA ACA ATG TGG GCC AGG                 726
Ile Val Ile Glu Gly Asp Ser Arg Thr Gly Ala Thr Met Trp Ala Arg
        575                 580                 585

TCT CTA GGC CCA CAT AAT TAT TTA TGT GGA CAT CTA GAC CTA AGC CCA                 774
Ser Leu Gly Pro His Asn Tyr Leu Cys Gly His Leu Asp Leu Ser Pro
    590                 595                 600

AAG GTG TAC AGT AAT GAT GCG TGG TAC AAC GTC ATT GAT GAC GTA GAC                 822
Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn Val Ile Asp Asp Val Asp
605                 610                 615                 620

CCG CAT TAT TTA AAG CAC TTC AAG GAA TTC ATG GGG GCC CAG AGG GAC                 870
Pro His Tyr Leu Lys His Phe Lys Glu Phe Met Gly Ala Gln Arg Asp
                625                 630                 635

TGG CAA AGC AAC ACA AAG TAC GGG AAG CCC ATT CAA ATT AAA GGG GGA                 918
Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro Ile Gln Ile Lys Gly Gly
            640                 645                 650

ATT CCC ACT ATC TTC CTC TGC AAT CCA GGA CCT ACC TCC TCA TAT AGG                 966
Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly Pro Thr Ser Ser Tyr Arg
        655                 660                 665

GAA TAT CTA GAC GAA GAA AAA AAC ATA TCC TTG AAA AAT TGG GCT CTC                 1014
Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser Leu Lys Asn Trp Ala Leu
    670                 675                 680

AAG AAT GCA ACC TTC GTC ACC CTC TAC GAG CCA CTG TTC GCA AGT ATC                 1062
Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu Pro Leu Phe Ala Ser Ile
685                 690                 695                 700

AAT CAA GGT CCA ACA CAA GAT AGC CAA GAA GAA ACC AAT AAG GCG TAA                 1110
Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu Glu Thr Asn Lys Ala  *
                705                 710                 715
```

GCGTGTAGAC CTAGACTGTG GCTGCTCATA GTACC

1145

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Pro Arg Leu Phe Lys Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr
1 5 10 15

Pro Asn Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys
20 25 30

Leu Glu Thr Pro Thr Asn Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu
35 40 45

His Glu Asn Gly Glu Pro His Leu His Val Leu Ile Gln Phe Glu Gly
50 55 60

Lys Tyr Gln Cys Lys Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Asn
65 70 75 80

Arg Ser Ala His Phe His Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr
85 90 95

Asp Val Lys Thr Tyr Val Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly
100 105 110

Val Ser Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala
115 120 125

Asn Asp Ala Tyr Ala Glu Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala
130 135 140

Leu Asn Ile Leu Lys Glu Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe
145 150 155 160

His Asn Leu Ser Ser Asn Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu
165 170 175

Val Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asn Gln Val Pro Asp
180 185 190

Glu Leu Glu Glu Trp Val Ala Glu Asn Val Val Tyr Ser Ala Ala Arg
195 200 205

Pro Trp Arg Pro Ile Ser Ile Val Ile Glu Gly Asp Ser Arg Thr Gly
210 215 220

Ala Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn Tyr Leu Cys Gly
225 230 235 240

His Leu Asp Leu Ser Pro Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn
245 250 255

Val Ile Asp Asp Val Asp Pro His Tyr Leu Lys His Phe Lys Glu Phe
260 265 270

Met Gly Ala Gln Arg Asp Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro
275 280 285

Ile Gln Ile Lys Gly Gly Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly
290 295 300

Pro Thr Ser Ser Tyr Arg Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser
305 310 315 320

Leu Lys Asn Trp Ala Leu Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu
325 330 335

Pro Leu Phe Ala Ser Ile Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu
340 345 350

Glu Thr Asn Lys Ala *
355

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: C1V2101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCCCACATT GTTGCGCCTG TTCTGC 26

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Yellow Leaf Curl Virus
(B) STRAIN: Israel

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 37..1110

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Navot, N
Pichersky, R
Zeidan, D
Zamir, D
Czosnek, H
(B) TITLE: Tomato yellow leaf curl virus: A whitefly-transmitted geminivirus with a single genomic component.
(C) JOURNAL: Virology
(D) VOLUME: 185
(F) PAGES: 151-168
(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC ATG CCT CGT TTA TTT AAA        54
                                        Met Pro Arg Leu Phe Lys
                                            360

ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAT TGT TCT CTC TCT       102
Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser
365                 370                 375                 380

AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT       150
Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn
                385                 390                 395

AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA       198
Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro
            400                 405                 410

CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC       246
His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn
        415                 420                 425

CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT       294
Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His
    430                 435                 440

CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG       342
Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val
445                 450                 455                 460

GAG AAA GAC GGA AAC TTC ATT GAT TTT GGA GTT TCC CAA ATC GAT GGC       390
Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly
                465                 470                 475
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```
AGA TCA GCT AGA GGA GGT CAG CAA TCT GCC AAC GAC GCA TAT GCC GAA      438
Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp Ala Tyr Ala Glu
            480                 485                 490

GCA CTC AAT TCA GGC AGT AAA TCC GAG GCC CTC AAT ATA TTA AAA GAG      486
Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala Leu Asn Ile Leu Lys Glu
        495                 500                 505

AAG GCC CCA AAG GAC TAT ATT TTA CAA TTT CAT AAT TTA AGT TCA AAT      534
Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe His Asn Leu Ser Ser Asn
    510                 515                 520

TTA GAT AGG ATT TTT AGT CCT CCT TTA GAA GTT TAT GTT TCT CCA TTT      582
Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu Val Tyr Val Ser Pro Phe
525                 530                 535                 540

CTT TCT TCT TCT TTT AAT CAA GTT CCA GAT GAA CTT GAA GAG TGG GTC      630
Leu Ser Ser Ser Phe Asn Gln Val Pro Asp Glu Leu Glu Glu Trp Val
                545                 550                 555

GCC GAG AAC GTC GTG TAT TCC GCT GCG CGG CCA TGG AGA CCC ATA AGT      678
Ala Glu Asn Val Val Tyr Ser Ala Ala Arg Pro Trp Arg Pro Ile Ser
            560                 565                 570

ATT GTC ATT GAG GGT GAT AGC AGA ACA GGC AAA ACA ATG TGG GCC AGG      726
Ile Val Ile Glu Gly Asp Ser Arg Thr Gly Lys Thr Met Trp Ala Arg
        575                 580                 585

TCT CTA GGC CCA CAT AAT TAT TTA TGT GGA CAT CTA GAC CTA AGC CCA      774
Ser Leu Gly Pro His Asn Tyr Leu Cys Gly His Leu Asp Leu Ser Pro
    590                 595                 600

AAG GTG TAC AGT AAT GAT GCG TGG TAC AAC GTC ATT AGA GAC GTA GAC      822
Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn Val Ile Arg Asp Val Asp
605                 610                 615                 620

CCG CAT TAT TTA AAG CAC TTC AAG GAA TTC ATG GGG GCC CAG AGG GAC      870
Pro His Tyr Leu Lys His Phe Lys Glu Phe Met Gly Ala Gln Arg Asp
                625                 630                 635

TGG CAA AGC AAC ACA AAG TAC GGG AAG CCC ATT CAA ATT AAA GGG GGA      918
Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro Ile Gln Ile Lys Gly Gly
            640                 645                 650

ATT CCC ACT ATC TTC CTC TGC AAT CCA GGA CCT ACC TCC TCA TAT AGG      966
Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly Pro Thr Ser Ser Tyr Arg
        655                 660                 665

GAA TAT CTA GAC GAA GAA AAA AAC ATA TCC TTG AAA AAT TGG GCT CTC     1014
Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser Leu Lys Asn Trp Ala Leu
    670                 675                 680

AAG AAT GCA ACC TTC GTC ACC CTC TAC GAG CCA CTG TTC GCA AGT ATC     1062
Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu Pro Leu Phe Ala Ser Ile
685                 690                 695                 700

AAT CAA GGT CCA ACA CAA GAT AGC CAA GAA GAA ACC AAT AAG GCG TAA     1110
Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu Glu Thr Asn Lys Ala  *
                705                 710                 715
```

GCGTGTAGAC CTAGACTGTG GCTGCTCATA CTACC

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Pro Arg Leu Phe Lys Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr
1 5 10 15

Pro Asn Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys
20 25 30

Leu Glu Thr Pro Thr Asn Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu
35 40 45

His Glu Asn Gly Glu Pro His Leu His Val Leu Ile Gln Phe Glu Gly
50 55 60

Lys Tyr Gln Cys Lys Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Asn
65 70 75 80

Arg Ser Ala His Phe His Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr
85 90 95

Asp Val Lys Thr Tyr Val Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly
100 105 110

Val Ser Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala
115 120 125

Asn Asp Ala Tyr Ala Glu Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala
130 135 140

Leu Asn Ile Leu Lys Glu Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe
145 150 155 160

His Asn Leu Ser Ser Asn Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu
165 170 175

Val Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asn Gln Val Pro Asp
180 185 190

Glu Leu Glu Glu Trp Val Ala Glu Asn Val Val Tyr Ser Ala Ala Arg
195 200 205

Pro Trp Arg Pro Ile Ser Ile Val Ile Glu Gly Asp Ser Arg Thr Gly
210 215 220

Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn Tyr Leu Cys Gly
225 230 235 240

His Leu Asp Leu Ser Pro Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn

245 250 255

Val Ile Arg Asp Val Asp Pro His Tyr Leu Lys His Phe Lys Glu Phe
260 265 270

Met Gly Ala Gln Arg Asp Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro
275 280 285

Ile Gln Ile Lys Gly Gly Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly
290 295 300

Pro Thr Ser Ser Tyr Arg Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser
305 310 315 320

Leu Lys Asn Trp Ala Leu Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu
325 330 335

Pro Leu Phe Ala Ser Ile Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu
340 345 350

Glu Thr Asn Lys Ala *
355

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: C1V2000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGGTCTACGT CTCTAATGAC GTTGTACC 28

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE
(A) ORGANISM: PTYC2V1439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTTGTGGAT CCCATTACCT TCCTGATGTT GTGG 34

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PTYARIv466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTAGGATCCT ATATCTGTTG TAAGGGC 27

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PTYARIc1046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTAACTAATG CAGGATCCTA CATTCCAGAG GGC 33

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PTYC2c1814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAACGGATCC TTGAAAAATT GGGC 24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PYTV1v1164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTACGAGAAC CATACTGAAA ACGCCT 26

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PTYC1c2196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAATCTGCAG ATGAACTAGA AGAGTGGG 28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer PTYC3c1320"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGTTCTGCAG CAGAGCAGTT GATCATGTAT TG 32

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer PTYC1v2182"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TAGGCCATGG CCGCGCAGCG GAATACACG 29

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer PTYC1V2406"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGTTCTGCAG CTTCGGCATA TGCGTCGT 28

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer PTYC1c2140"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATTTCCATGG AGACCCATAA GTATTGTC 28

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer PTYCv1707"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGTAGTATGA GGATCCACAG TCTAGGTCT 29

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bean Golden Mosaic Geminivirus

B STRAIN: Type II Isolates
C: INDIVIDUAL ISOLATE: Guatemala

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1062

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Faria, JC
Gilbertson, RL
Hanson, SF
Morales, FJ
Ahlquist, P
Loniello, AO
Maxwell, D
(B) TITLE: Bean Golden Mosaic Geminivirus Type II Isolates from the Dominican Republic and Guatemala: Nucleotide Sequences, Infectious Pseudorecombinants, and Phylogenetic Relationships
(C) JOURNAL: Phytopathology
(D) VOLUME: 84
(E) ISSUE: 3
(F) PAGES: 321-329
(G) DATE: 1994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC          48
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
    360                 365                 370

ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT          96
Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
375                 380                 385                 390

CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG         144
Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
                395                 400                 405

GAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC         192
Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
            410                 415                 420

GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC         240
Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
        425                 430                 435

TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA         288
Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
    440                 445                 450

AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA         336
Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
455                 460                 465                 470

TGG GGA CAA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG         384
Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
                475                 480                 485

TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA         432
```

```
Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
          490                 495                 500

TCT GCC TTG ACA ATA TTG AAG GAA GAA CAA CCG AAA GAT TAC GTC CTT      480
Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
     505                 510                 515

CAA CAT CAC AAC ATC CGT TCT AAT CTC GAA CGG ATC TTC GTC AAA GTG      528
Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
 520                 525                 530

CCG GAA CCA TGG GTT CCT CCA TTT CCG TTG TCA TCA TTC ATC AAT GTT      576
Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
535                 540                 545                 550

CCG GTT GTT ATG CAA GAA TGG GTT GAC GAC TAT TTC GGA AGG GGT TCC      624
Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
                555                 560                 565

GCT GCG CGG CCG GAA AGA CCT ATT AGT ATC ATC GTC GAA GGT GAT TCA      672
Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
          570                 575                 580

CGA ACC GGA AAG ACA ATG TGG GCT CGT GCA TTA GGA CCA CAT AAT TAT      720
Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
     585                 590                 595

TTG AGC GGT CAT TTG GAC TTT AAT TCA CGT GTC TAT TCC AAC GCA GTG      768
Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
 600                 605                 610

GAA TAC AAC GTC ATT GAT GAC ATA AGC CCC AAT TAT TTG AAG TTA AAG      816
Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
615                 620                 625                 630

CAC TGG AAA GAA CTA ATT GGG GCA CAA AAG GAC TGG CAA TCT AAC TGT      864
His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
                635                 640                 645

AAA TAT GGA AAG CCG GTT CAA ATT AAA GGA GGA ATA CCA TCA ATC GTG      912
Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
          650                 655                 660

TTG TGC AAT CCA GGT GAG GGT TCC AGT TAT AAA GAC TTC CTC GAC AAA      960
Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
     665                 670                 675

GAA GAA AAC CGA GCT TTA CAC AAC TGG ACT ATT CAT AAT GCG ATC TTC     1008
Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
 680                 685                 690

GTC ACC CTC ACA GCC CCC CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA     1056
Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
695                 700                 705                 710

ACG TAG AGCCATTCGT CGACGACGCA TTGACTTGAA CTGCGGCTGT TCCATATTTT      1112
Thr  *

ACCATATCAA GTGCGCAGAT CATGGATTCA CGCACAGGGG AGAACATCAC TGCGCATCAG  1172
```

GCAGAGAATT C

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
 1               5                  10                  15

Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
            20                  25                  30

Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
        35                  40                  45

Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
    50                  55                  60

Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
65                  70                  75                  80

Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85                  90                  95

Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
            100                 105                 110

Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
        115                 120                 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
    130                 135                 140

Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
145                 150                 155                 160

Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
                165                 170                 175

Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
            180                 185                 190

Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
        195                 200                 205

Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
    210                 215                 220

Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225                 230                 235                 240
```

```
Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
                245                 250                 255

Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
            260                 265                 270

His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
        275                 280                 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
    290                 295                 300

Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
305                 310                 315                 320

Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
                325                 330                 335

Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
            340                 345                 350

Thr *
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bean Golden Mosaic Geminivirus
(B) STRAIN: Type II
(C) INDIVIDUAL ISOLATE: Guatemala

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC      48
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
355                 360                 365                 370

ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT      96
Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
                375                 380                 385

CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG     144
Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
```

```
                    391                 395                 400

GAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC      192
Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
        405                 410                 415

GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC      240
Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
    420                 425                 430

TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA      288
Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
435                 440                 445                 450

AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA      336
Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
                455                 460                 465

TGG GGA CAA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG      384
Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
            470                 475                 480

TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA      432
Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
        485                 490                 495

TCT GCC TTG ACA ATA TTG AAG GAA GAA CAA CCG AAA GAT TAC GTC CTT      480
Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
    500                 505                 510

CAA CAT CAC AAC ATC CGT TCT AAT CTC GAA CGG ATC TTC GTC AAA GTG      528
Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
515                 520                 525                 530

CCG GAA CCA TGG GTT CCT CCA TTT CCG TTG TCA TCA TTC CGC AAT GTT      576
Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Arg Asn Val
                535                 540                 545

CCG GTT GTT ATG CAA GAA TGG GTT GAC GAC TAT TTC GGA AGG GGT TCC      624
Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
            550                 555                 560

GCT GCG CGG CCG GAA AGA CCT ATT AGT ATC ATC GTC GAA GGT GAT TCA      672
Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
        565                 570                 575

CGA ACC GGA AAG ACA ATG TGG GCT CGT GCA TTA GGA CCA CAT AAT TAT      720
Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
    580                 585                 590

TTG AGC GGT CAT TTG GAC TTT AAT TCA CGT GTC TAT TCC AAC GCA GTG      768
Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
595                 600                 605                 610

GAA TAC AAC GTC ATT GAT GAC ATA AGC CCC AAT TAT TTG AAG TTA AAG      816
Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
                615                 620                 625

CAC TGG AAA GAA CTA ATT GGG GCA CAA AAG GAC TGG CAA TCT AAC TGT      864
His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
```

```
                630                 635                 640

AAA TAT GGA AAG CCG GTT CAA ATT AAA GGA GGA ATA CCA TCA ATC GTG      912
Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
        645                 650                 655

TTG TGC AAT CCA GGT GAG GGT TCC AGT TAT AAA GAC TTC CTC GAC AAA      960
Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
    660                 665                 670

GAA GAA AAC CGA GCT TTA CAC AAC TGG ACT ATT CAT AAT GCG ATC TTC     1008
Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
675                 680                 685                 690

GTC ACC CTC ACA GCC CCC CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA     1056
Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
                695                 700                 705

ACG TAG AGCCATTCGT CGACGACGCA TTGACTTGAA CTGCGGCTGT TCCATATTTT      1112
Thr  *

ACCATATCAA GTGCGCAGAT CATGGATTCA CGCACAGGGG AGAACATCAC TGCGCATCAG  1172

GCAGAGAATT C                                                       1183
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
 1               5                  10                  15

Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
            20                  25                  30

Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
        35                  40                  45

Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
    50                  55                  60

Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
65                  70                  75                  80

Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85                  90                  95

Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
            100                 105                 110

Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
```

```
                115                 120                 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
    130                 135                 140

Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
145                 150                 155                 160

Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
                165                 170                 175

Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Arg Asn Val
            180                 185                 190

Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
        195                 200                 205

Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
    210                 215                 220

Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225                 230                 235                 240

Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
                245                 250                 255

Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
            260                 265                 270

His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
        275                 280                 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
    290                 295                 300

Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
305                 310                 315                 320

Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
                325                 330                 335

Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
            340                 345                 350

Thr *
```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: SHGA191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CATCATTCCG CAATGTTCCG GT 22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bean Golden Mosaic Geminivirus
(B) STRAIN: Type II
(C) INDIVIDUAL ISOLATE: Guatemala

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC      48
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
355                 360                 365                 370

ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT      96
Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
                375                 380                 385

CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG     144
Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
            390                 395                 400

GAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC     192
Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
        405                 410                 415

GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC     240
Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
    420                 425                 430

TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA     288
Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
435                 440                 445                 450
```

```
AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA      336
Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
                455                 460                 465

TGG GGA CAA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG      384
Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
            470                 475                 480

TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA      432
Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
        485                 490                 495

TCT GCC TTG ACA ATA TTG AAG GAA GAA CAA CCG AAA GAT TAC GTC CTT      480
Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
    500                 505                 510

CAA CAT CAC AAC ATC CGT TCT AAT CTC GAA CGG ATC TTC GTC AAA GTG      528
Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
515                 520                 525                 530

CCG GAA CCA TGG GTT CCT CCA TTT CCG TTG TCA TCA TTC ATC AAT GTT      576
Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
                535                 540                 545

CCG GTT GTT ATG CAA GAA TGG GTT GAC GAC TAT TTC GGA AGG GGT TCC      624
Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
            550                 555                 560

GCT GCG CGG CCG GAA AGA CCT ATT AGT ATC ATC GTC AGA GGT GAT TCA      672
Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Arg Gly Asp Ser
        565                 570                 575

CGA ACC GGA AAG ACA ATG TGG GCT CGT GCA TTA GGA CCA CAT AAT TAT      720
Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
    580                 585                 590

TTG AGC GGT CAT TTG GAC TTT AAT TCA CGT GTC TAT TCC AAC GCA GTG      768
Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
595                 600                 605                 610

GAA TAC AAC GTC ATT GAT GAC ATA AGC CCC AAT TAT TTG AAG TTA AAG      816
Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
                615                 620                 625

CAC TGG AAA GAA CTA ATT GGG GCA CAA AAG GAC TGG CAA TCT AAC TGT      864
His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
            630                 635                 640

AAA TAT GGA AAG CCG GTT CAA ATT AAA GGA GGA ATA CCA TCA ATC GTG      912
Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
        645                 650                 655

TTG TGC AAT CCA GGT GAG GGT TCC AGT TAT AAA GAC TTC CTC GAC AAA      960
Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
    660                 665                 670

GAA GAA AAC CGA GCT TTA CAC AAC TGG ACT ATT CAT AAT GCG ATC TTC     1008
Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
675                 680                 685                 690
```

```
GTC ACC CTC ACA GCC CCC CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA      1086
Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
                695                 700                 705

ACG TAG
Thr  *                                                          1062
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
 1               5                  10                  15

Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
            20                  25                  30

Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
        35                  40                  45

Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
    50                  55                  60

Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
65                  70                  75                  80

Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85                  90                  95

Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
            100                 105                 110

Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
        115                 120                 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
    130                 135                 140

Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
145                 150                 155                 160

Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
                165                 170                 175

Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
            180                 185                 190

Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
        195                 200                 205
```

Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Arg Gly Asp Ser
210 215 220

Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225 230 235 240

Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
245 250 255

Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
260 265 270

His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
275 280 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
290 295 300

Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
305 310 315 320

Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
325 330 335

Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
340 345 350

Thr *

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: SHGA221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCATCGTCAG AGGTGATTCA C 21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

) TOPOLOGY: Circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bean Golden Mosaic Geminivirus
(B) STRAIN: Type II
(C) INDIVIDUAL ISOLATE: Guatemala

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC          48
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
355                 360                 365                 370

ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT          96
Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
                375                 380                 385

CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG         144
Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
            390                 395                 400

GAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC         192
Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
        405                 410                 415

GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC         240
Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
    420                 425                 430

TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA         288
Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
435                 440                 445                 450

AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA         336
Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
                455                 460                 465

TGG GGA CAA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG         384
Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
            470                 475                 480

TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA         432
Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
        485                 490                 495

TCT GCC TTG ACA ATA TTG AAG GAA GAA CAA CCG AAA GAT TAC GTC CTT         480
Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
    500                 505                 510
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CAA CAT CAC AAC ATC CGT TCT AAT CTC GAA CGG ATC TTC GTC AAA GTG      525
Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
515                 520                 525                 530

CCG GAA CCA TGG GTT CCT CCA TTT CCG TTG TCA TCA TTC ATC AAT GTT      575
Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
                535                 540                 545

CCG GTT GTT ATG CAA GAA TGG GTT GAC GAC TAT TTC GGA AGG GGT TCC      624
Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
            550                 555                 560

GCT GCG CGG CCG GAA AGA CCT ATT AGT ATC ATC GTC GAA GGT GAT TCA      672
Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
        565                 570                 575

CGA ACC GGA CAC ACA ATG TGG GCT CGT GCA TTA GGA CCA CAT AAT TAT      720
Arg Thr Gly His Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
    580                 585                 590

TTG AGC GGT CAT TTG GAC TTT AAT TCA CGT GTC TAT TCC AAC GCA GTG      768
Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
595                 600                 605                 610

GAA TAC AAC GTC ATT GAT GAC ATA AGC CCC AAT TAT TTG AAG TTA AAG      816
Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
                615                 620                 625

CAC TGG AAA GAA CTA ATT GGG GCA CAA AAG GAC TGG CAA TCT AAC TGT      864
His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
            630                 635                 640

AAA TAT GGA AAG CCG GTT CAA ATT AAA GGA GGA ATA CCA TCA ATC GTG      912
Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
        645                 650                 655

TTG TGC AAT CCA GGT GAG GGT TCC AGT TAT AAA GAC TTC CTC GAC AAA      960
Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
    660                 665                 670

GAA GAA AAC CGA GCT TTA CAC AAC TGG ACT ATT CAT AAT GCG ATC TTC     1008
Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
675                 680                 685                 690

GTC ACC CTC ACA GCC CCC CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA     1056
Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
                695                 700                 705

ACG TAG                                                             1062
Thr  *
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
1 5 10 15

Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
20 25 30

Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
35 40 45

Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
50 55 60

Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
65 70 75 80

Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
85 90 95

Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
100 105 110

Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
115 120 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
130 135 140

Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
145 150 155 160

Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
165 170 175

Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
180 185 190

Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
195 200 205

Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
210 215 220

Arg Thr Gly His Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225 230 235 240

Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
245 250 255

Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
260 265 270

His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
275 280 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
290 295 300

```
Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
305                 310                 315                 320

Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
                325                 330                 335

Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
            340                 345                 350

Thr *
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: SHGA228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAACCGGACA CACAATGTGG GC 22

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bean Golden Mosaic Geminivirus
(B) STRAIN: Type II
(C) INDIVIDUAL ISOLATE: Guatemala

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1062

xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC          48
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
355                 360                 365                 370

ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT          96
Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
                375                 380                 385

CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG         144
Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
            390                 395                 400

AAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC         192
Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
        405                 410                 415

GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC         240
Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
    420                 425                 430

TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA         288
Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
435                 440                 445                 450

AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA         336
Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
                455                 460                 465

TGG GGA CAA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG         384
Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
            470                 475                 480

TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA         432
Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
        485                 490                 495

TCT GCC TTG ACA ATA TTG AAG GAA GAA CAA CCG AAA GAT TAC GTC CTT         480
Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
    500                 505                 510

CAA CAT CAC AAC ATC CGT TCT AAT CTC GAA CGG ATC TTC GTC AAA GTG         528
Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
515                 520                 525                 530

CCG GAA CCA TGG GTT CCT CCA TTT CCG TTG TCA TCA TTC ATC AAT GTT         576
Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
                535                 540                 545

CCG GTT GTT ATG CAA GAA TGG GTT GAC GAC TAT TTC GGA AGG GGT TCC         624
Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
            550                 555                 560

GCT GCG CGG CCG GAA AGA CCT ATT AGT ATC ATC GTC GAA GGT GAT TCA         672
Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
        565                 570                 575

CGA ACC GGA AAG ACA ATG TGG GCT CGT GCA TTA GGA CCA CAT AAT TAT         720
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Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
    580                 585                 590

TTG AGC GGT CAT TTG GAC TTT AAT TCA CGT GTC TAT TCC AAC GCA GTG      763
Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
595                 600                 605                 610

GAA TAC AAC GTC ATT AGA GAC ATA AGC CCC AAT TAT TTG AAG TTA AAG      815
Glu Tyr Asn Val Ile Arg Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
                615                 620                 625

CAC TGG AAA GAA CTA ATT GGG GCA CAA AAG GAC TGG CAA TCT AAC TGT      864
His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
            630                 635                 640

AAA TAT GGA AAG CCG GTT CAA ATT AAA GGA GGA ATA CCA TCA ATC GTG      912
Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
        645                 650                 655

TTG TGC AAT CCA GGT GAG GGT TCC AGT TAT AAA GAC TTC CTC GAC AAA      960
Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
    660                 665                 670

GAA GAA AAC CGA GCT TTA CAC AAC TGG ACT ATT CAT AAT GCG ATC TTC     1008
Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
675                 680                 685                 690

GTC ACC CTC ACA GCC CCC CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA     1056
Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
                695                 700                 705

ACG TAG                                                             1062
Thr  *
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu
 1               5                  10                  15

Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu
            20                  25                  30

Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu
        35                  40                  45

Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe
    50                  55                  60

Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser
```

65 70 75 80

Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser
85 90 95

Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu
100 105 110

Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
115 120 125

Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu
130 135 140

Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu
145 150 155 160

Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val
165 170 175

Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val
180 185 190

Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser
195 200 205

Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser
210 215 220

Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr
225 230 235 240

Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val
245 250 255

Glu Tyr Asn Val Ile Arg Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys
260 265 270

His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys
275 280 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val
290 295 300

Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys
305 310 315 320

Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe
325 330 335

Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln
340 345 350

Thr *

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: SHGA262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ACGTCATTAG AGACATAAGC 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato-Infecting Geminivirus from Gautemala (TGV-GA1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AGATGAAGCT ATTGAAATGC TTCAAAATCT GCCATGGTCA GTCGTCAAAC CAACGTACAT 60

ACGAGTCGCC AGAGAGGAAC ACGCAGATGG ATTTCCGCAC CTCCACTGTC TCATCCAACT 120

CTCCGGGAAG TCCAACATCA AGGATGCTAG ATTTTTCGAC CTCACTCACC CAGAAGGTCT 180

GCCAATTTTC ATCCAAAC 198

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato-Infecting Geminivirus from Guatemala (TGV-GA1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGGGTTCCGT GGCATTTTTG CAAATATGAG CCAGGACACC AGGGGGAGCT CTCTCTAAAA 60

CTTTATTTTG CTGGTGTCCT GGTGTCCCAT TTATACTAAA ACCCTCTTGG GGACACCAAG 120

GGCAAATTCG GCCATCCGCA ATAATATTAC CGGATGGCCG CGATTTTTTT TGGACCTGGC 180

CCACTATCAG AAATTGCGTT GGGCCTTTCT GGATAAGTTA ACCAATCAAT ACACGTTTGG 240

GTAGTCTAAT TATTACAACT TGGTCACCAA GTTGTTTTAT GGTCTATAAA TTTGTCGTTA 300

TGTGTGTGGT CCAACCACGT AAATATTGAT AATGCCTAAG CGTGATGCCC CATGGCGCTT 360

AATGGCGGGT ACCCTAAGG 379

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato Leaf Curl Geminivirus from Southern India

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACCGGATGGC CGCGATTTTT TTTGTGGGCC CCTCAACGCA CTAACTGACA AGGACATGCT 60

AACCAATCAC ATGACGCGCT CAAAGCTTAA TTGTTTTGTG GTCCCCTATT TAAACTTCGG 120

CACCAAGTAT TGTATTTTGC ACTATGTGGG ATCCATTGTT AAACGAGTTT CCTGAAACCG 180

TTCACGGTTT TAGATGTATG TTAGCAGTTA AATATCTGCA ATTAGTAGAA AAGACCTATT 240

CTCCCGACAC ATTAGGTTAC GATTTAATTA GGGATTTAAT TTCAGTTATT AGGGCTAGAA 300

ATTATGTCGA AGCGACCAGC AGATATAATC ATTTCCACTC CCGCTTCGAA GGTACGTCGC 360

CGTCTCAACT TCGACAGCCC ATATGTGAGC CGTGCTGTTG CCCCCATTGT CCGCGTCACC 420

AAAGCAAAAG CATGGGCGAA CAGGCCCATG AACAGAAAGC CCAGGATGTA CAGGATGTAC 480

AGAAGTCCAG ATGTCCCTAG AGGATGTGAA GGCCCATGTA AGGTCCAGTC GTTTGAGTCC 540

AGACACGATG TAGTCCATAT AGGCAAGGTC ATGTGTATTA GTGATGTCAC TCGTGGAACC 510
GGGCTGACCC ATAGAGTTGG TAAGCGTTTT TGTGTTAAGT CTGTTTACGT TTTGGGGAAG 660
ATATGGATGG ACGAAAATAT AAAGACCAAG AATCATACGA ACAGTGTCAT GTTTTTTCTT 720
GTTCGTGACC GTCGTCCTGT TGACAAGCCA CAAGACTTTG GAGAGGTGTT CAATATGTTT 780
GACAACGAGC CTAGCACTGC TACTGTTAAG AATATGCACA GAGATCGTTA TCAGGTGTTG 840
AGGAAGTGGC ATGCAACTGT CACCGGTGGA CAGTACGCTT CAAAGGAACA GGCATTAGTG 900
AAGAAGTTTG TTAGGGTTAA TAATTATGTT GTTTATAACC AGCAAGAGGC TGGGAAATAT 960
GAGAATCATA CTGAAAATGC ATTGATGTTG TATATGGCGT GTACTCACGC CTCTAACCCT 1020
GTGTATGCTA CTTTGAAGAT ACGGATCTAT TTTTATGATT CAGTATCGAA TTAATAAATA 1080
TTGAATTTTA TTGAATATGT TTGGTCTACA TATACAACGT GGTGTAATAC ATTCCATAAT 1140
ACATAATCAA CGGCTCTGAT TACATTGTTA ATACTGATAA CTCCTAAATT ATTTAAGTAC 1200
TTAAGCACTT GGGTCTTAAA TACCCTTAAG AAGCGACCAG TCGGAGGCTG TGAGGTCATC 1260
CGGATTCGGT AGATTAGGAA ACATTTGTGT ATCCCCAACA CTTTCCTCAG GTTGTGATTG 1320
AACTGTACTT GGTCGGTGAT GATGTCTTGG TTCATCAGGA ATGGCCGGTT GTGATGCTCT 1380
GTTATCTTGA AATATAGGGG ATTTTGAATC TCCCAGATAA ACACGCCATT CTCTGCTTGA 1440
GCTGCAGTGA TGAGTTCCCC TGTGCGTGAA TCCATGGTCG TGGCAGGCTA ATGCTATGAA 1500
GTAAGAACAG CCGCACGGTA GATCAACTCG TCGACGTCTG GTCCCCTTCT TGGCTAGCCT 1560
GTGCTGCACT TTGATTGGTA CCTGAGTAGA GTGGGCCTTC GAGGGTGACG AAGGTCGCAT 1620
TCTTTATAGC CCAGAATTTT AGTTTAGAAT TCTTTTCTTC ATCCAAGAAT TCTTTATAGC 1680
TGGAGTTGGG TCCTGGATTG CAGAGGAAGA TTGTGGGAAT TCCGCCTTTA ATTTGAACTG 1740
GCTTATTGTA CTTTCTATTT GATTGCCAGT CCCTTTGGGC CCCCATGAAT TCCTTAAAGT 1800
GCTTTAGGTA GTTGGGGTCT ACGTCATCAA TTACGTTATA CCACGCATCA TTACTGTAGA 1860
CCTTTGGGCT AAGGTCTAGA TGACCACACA AATAATTATG TGGTCCCAGT GATCTGGCCC 1920
ACATAGTCTT GCCGGTCCTA CTGTCACCCT CAATCACTAT ACTTACGGGC CTCAAAGGCG 1980
CGCACCTGAC GACGTTCTCG GCAGCCCACT CTTCAAGTTC ATCTGGAACT TGATCAAAGG 2040
AAGAAGAAGA AAAAGGAGAA GCATAAACCT CCATTGGAGG TGTAAAAATC CTATCTAAAT 2100
TACATTTTAA ATTATGATAT TGAAAAATAA AATCTTTAGG GAGTTTTTCC CTAATTATTG 2160
CTAAAGCTGC TTCAGCTGAA CCTGCATTTA AGGCCTCTGC GGCAGCATCA TTAGCTGTCT 2220
GTTGACCTCC TCGTGCAGAT CTTCCATCGA TCTGAAACTC ACCCCAGTCG ATGTAATCAC 2280
TGTCCTTCTC GATGTAGGAC TTGACATCGG AGCTGAGCTT AGCTCCCTGG AAGTTTGGAT 2340

GGAATTGGGT GGAGTTATTA GGGTGAGTGA CATCGAAATG TCTGGGGTTT CGGAACTTGG 2400

ATTTACCCTT GAATTGGATG AGGGCATGGA TATGCATAGA CCCATCTTGG TGTTTCTCTT 2460

GGGCTACTCT GATAAATAAT TTATCAGATG GACAGAAAAT GTTTTTAAGG ATTTCGAGCA 2520

TTTGTTCTTT GGGTATTGGG CATTTGGGAT AAGTAAGGAA GATATTTTTG GCATTAACAC 2580

AAAAAGAGTT AATACGAGGC ATATTGAATT GGGGACACTC AAAACTCTGA GGAATGGGGG 2640

ACTCGGGGGA CGCATTTATA AGGCGTCCCT AAATGGCATT TTTGTAATTT GGGAAAGTAA 2700

TTCAAAATCC TCACGCTCCA AAAAGCGGCC ATCCGTATAA TATT 2744

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato-Infecting Geminivirus from Mexico
(Chino-like sympts)

(ix) FEATURE:
(A) NAME/KEY: unsure
(B) LOCATION: 1220..1403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAAGGTGGTC CGATATATCC TGGGCTTGGT GTACATGGGC CTGTTAATTT AACGAGCGGC 60

CTTATCGAAT TTAGGGCCCA TACCCGTGCC ACGTGAATAA TTAGCAGGCG GGAAACCTTG 120

GAGGTCCCCG CCATTAAACG CCATGGGGCA TCCCGCTTGG CCATTTTGAA TTAAAGATAT 180

AAATGCACAT GCACGTGCAT TTATAGGACC ACACCTTGGT CACCAAGGCA CAAATATCTA 240

GACTTGACAG CCGGGATGTG ATTGGTCAGT CAAAATCAAA TAATTGGTGG TCCCATCTCT 300

TTATCTCTTT AATCTCAGCC CTCTATTCTG AGTGGTCCCC CAGATACTCC AAAAAATCGC 360

GGCCATCCGG TAATATTATA GGATGGCCGC TTTTGCCCCT GGAGTTCCCC CTGTGTGTTC 420

TAGTATTTAA GGGACTCCAG GACTCCAGAA ACATAGTACG GTTTTATGAG GCACTCTCCT 480

GGAGTCCTAC ACCATATTTG CGAAAATGCC ACTACCCCCA AAGTCATTTC GTTTACAATG 540

TAAAAACATT TTCTTAACAT ATCCACAATG CGATATCCCA AAGGATGAAG CTCTCGAAAT 600

GCTGCAGTCG TTAAAAATGG TCTGTCGTAA AACCCATATA CATAAGGGTA TCACGGGAGG 660

AGCATTCCGA TGGGTTTCCG CACTTGCACT GTCTCATCCA GCTAACTGGA AAGTGCAACA 720

TCAAAGATGC TCGGTTCTTC GACATTACTC ACCCCCGGAG ATCTGGCCAG TTTCATCCAA 780

ACGTTCAGGC GGCTAAAGAC ACAAATGCCG TAAAGAATTA TATCACTAAA GATGGCGATT 840

ATTGCGAATC TGGAAAGTAC AAAGTTTCCG GGGGTTCCAA AGCAAATAAA GACGACGTCT 900

ACCATAACGC TGTAAATGCA GCAAGTGCGA CAGAGGCGCT CGACATTATA AGGCTGGAGA 960

TCCAAGAACG TTCATTGTCA GCTATCATAA CGTTAAGTCT AACATCGAGC GCCTGTTCAA 1020

ACCTCCTCCT AAACCATGGA CTCCTCCTTA TCCAATTTCC TCGTTTAATA ACGTTCCTGA 1080

GGATATGCAA ACTTGGGTTG CTGAATATCT TGGTCGGACT TCCGCTGCGC GGCCAGATAG 1140

ACCGATTAGT ATTGTCATTG AGGGCGATTC GCGAAGGCAA GACAATGTGG GCACGTGCAT 1200

TAGGCCCACA TAATTATTTG AGTGTCACCT TGATTTCAAT TCAAAAGTCT ATTCAAACGA 1260

TGTGGAGTAT AACGTCATTG ATGATATCAC GCCCATTATC TAAAGTTGAA ACCTGGAAAG 1320

AGCTTATTGG GGCCCAAAGG GACTGGCAGT CCAACTGTAA ATCGGAAACC AGTTCAAATT 1380

AACGCCGGGA TTCCATCAAT TGT 1403

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato-Infecting Geminivirus similar to Pepper Hausteco
(C) INDIVIDUAL ISOLATE: Sinaloa, Mexico

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Torres-Pacheco, I
Garzon-Tiznado,
Herrera-Estrella, L
Rivera-Bustmante, R
(B) TITLE: Sequence from a new tomato-infecting geminivirus from Sinaloa, Mexico with some similarity to Pepper Hausteco Virus
(C) JOURNAL: J. General Virology
(D) VOLUME: 74
(F) PAGES: 2225-2231
(G) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCTGAATGT TCGGATGGAA ATGTGCTGAT CTGGTTGAGG ATACGAGGTC AAAGAATCTG 60

TTGTTCGTGC ATTGGTATTT TCCTTCGAAC TGAATAAGCA CGTGCAGATG AGGTTGCCCA 120

TCTTCATGAG ATTCTTTGCA AATTTTGATG TACTTCTTGT TTACCGGCGT CGAGAGGTTT 180

TGTAGTTGAG CGAGAGCCTC TTCTTTGGAA ATGGAACATT GGGGATAGGT GAGGAAATAA 240

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ACCGATTGGA GCTCTTTAAC CTGAGCTTAT TGTATCGGTG TATTGGTAGC CAATATATAG 360

TATATGGGAG TTATCTAGGA TCTTCGTACA CGTGGAGGCC ATCCGTTATA ATATTACCGG 420

ATGGCCGACC GCTTACCTTA TCTATCCGTA CAGCTTTATT TTGAATTAAA GATGTTACTT 480

TTATGCTATC CAATGAGCGT GCGTCTGGGA AGCTTAGTTA ACCGTTCCAG ACGTGGGGAC 540

CAAGTAGTGT ATGACCACTT TATTGACTGT CAGCTTTATA AATTCAAATT AACACATAAG 600

TGGTCCATAT ACCTTTAATT CAAAATGCCT AAGCGTGATG CTCCTTGGCG ATTAACGGCG 660

GGGACCGCAA GATTAGCCGA ACTGGCAATA ATTCACGGGC TCTTATCATG GGCCCGAGTA 720

CTAGCAGGGC CTCAGCTTGG GTTAATCGCC CAATGTACAG GAAGCCCCGC ATTTATCGTA 780

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato-Infecting Geminivirus similar to Pepper Hausteco
(C) INDIVIDUAL ISOLATE: Sinaloa, Mexico

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TTTTATATTC AAAAGATATT TGGATTTTAA TATTAGCAAT TACAAATAAG CAATTTAATA 60

TGTATTCCAC TAGGTTTAGA CGTGGGTTAT CGTATGGTCC ACGTCGTTCT AATGCACGTA 120

ATTATGGTTT TAAACGCACA TTGGCCGTTA AGCGTTTTGA TGGTAATCGG CGCCAGAAGC 180

AAGTGAAGAA AACCGATGAA GAGTTAAAAA TGTCATCGCA GCGTATGCAT GAAAATCAGT 240

ATGGTCCAGA TTTTGTAATG GCGCATAACA CATCAATATC TACGTTCATC AATTTCCCAC 300

AAATGTGTAA GACTCAGCCC AATCGTAGCA GGTCCTATAT TAAGTTAAAA TGTTTGCATT 360

TTAAGGGAAC CGTTAAGATT GAACGTGTTG GGGCTGAGTT AAATATGGCC GGGTTAAGTC 420

CAAAGATTGA GGGAGTTTTC ACCGTGGTTG TTGTTGTTGA CCGTAAGCCG CATTTGAGTC 480

CCACTGGCAA CTTGCACACA TTTGATGAGT TATTTGGTGC AAGAATTCAT AGTCATGGTA 540

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TTATCTCCGT TGAGAAGGAC ACTATGATGC TGGATCTAGA AGGATCCACG TGCCTGTCTA 660

ATCGGCGTTT TAATTGTTGG TCCACATTTA AGGACCTGGA TCCTTCATCA TGTAACGGCG 720

TCTATGACAA TATAAGTAAA AACGCCTTGT TAGTTTATTA TTGCTGGATG TCGGATGCTA 780

TGTCTAAGGC ATCCACATTT GTATCATTTG ATTTGGACTA TGTTGGTTGA GAAATAATAA 840

ACTTGCGCAC TTTGCTCAAA TCTTTATTTT GTCACAAAAT AATATATTTA TTTCAACGAC 900

TTAGGCTGTG TCGGATTACA ATTACTGTTA ATACATTCAT GGACCGTAGT CCTTCAAGTT 960

CATTTAATTG GGCCAAGGAC ATAGTTATAT TTGAGTGGGT TCGTGTTAGA CCAACTTGTG 1020

ATGCTGAATC ACCTGGGTCT AGAACACTTC CGCCTAACTG ATGAAGATCT TTATACGGAT 1080

GTAATGCGCT ATGTCCTTGG GAGTCGGGAT TTGTGTGAGT GGTTGCTATG GTGCTTCTAC 1140

ATGCCCATGA TTCACCCGGT TTTAATTCAA TTGGGCCTGT AATGCCGAAC CTTGACATTG 1200

ATGCTGACCT CAATGG 1216

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Tomato-Infecting Geminivirus similar to Pepper Hausteco
(C) INDIVIDUAL ISOLATE: Sinoloa, Mexico

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AAATATCTAA CGTTTCAGGG GTGGTAGAGG ACGCTCCACG TCATTACACA TTTCTCCATG 60

TATGGACCAC ACTTTAATTT GAAATGAAGG CGCGCGATTG AACTCATCCA ACGACCCACA 120

TGATGCCACG TACACATAAC TCATAGTGCG CGCCAGCTGT ACCAAAGGAA AGAGAGTGGA 180

AGCGGTCGGC CATCCGGTAA TATTATAACG GATGGCCTCC ACGTGTACGA AGATCCTAGA 240

TAACTCCCAT ATACTATATA TTGGCTACCA ATACACCGAT ACCATCAGCA CAGGTTAAAG 300

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AAAACCAGCT GCCAATTCTA TATAACGCAG CTGCATGTTC ATTAAATTAA TCATACTAAT 420
TCTCTCTTCT CTCTCTTCTT CAGACGCTCT TGCTTGCTTC CTCACCGGTT TCTTCATAAA 480
TTCTTCATAG AATAGCAATA TCTTAACATC GAAGTAAGCT TATTTTTTGA ACTCTTTCAG 540
CAAATAATAA TTTGTCATTT TCGTTACCAT TATCATTGTT AGGTATAGCT TCTTATTGGC 600
AGCTTCATAC TCGGTAAGCC TTCAGCTGCG CAGCCAATTT TTCATATATG GATTCTAGGT 660
TGGCGAATCC TCCTAGTGCC TTCAATTATA TAGAATCCCA TAGAGATGAA TATCAGCTCT 720
CTCATGACTT AACTGAAATA GTACTTCAAT TTCCGTCAAC GGCGTCACAG TACGCAGCCA 780
GACTTAGTCG TAGCTGTATG AAAATTGACC ATTGCGTTAT CGAGTATAGA CAGCAGGTTC 840
CGATAAACGC AACTGGATCG GTAATAGTGG AAATCCATGA CAAGAGAATG ACTGACAATG 900
AATCATTACA AGCTTCCTGG ACATTTCCAC TAAGATGCAA CATTGATCTC CATTACTTCT 960
CGGCGTCCTT CTTCTCCTTG AAGGACCCCA TACCATGGAA GCTATATTAC CGGGTCTCAG 1020
ATACTAACGT ACATCAGAAC ACACATTTTG CCAAGTTCAA AGGCAAATTG AAGTTGTCCA 1080
CAGCTAAACA CTCTGTGGAT ATACCCTTCA 1110

WE CLAIM:

1. A transgenic plant comprising chromosomal DNA, the plant harboring geminivirus DNA integrated into the chromosomal DNA, the geminivirus DNA encoding a protein required for geminivirus replication, and the geminivirus DNA conferring resistance to viral infection.

2. Transgenic plants according to claim 1 in which the geminivirus DNA is wild type DNA.

3. The transgenic plant according to claim 1 in which the geminivirus DNA comprises an ORF selected from the group consisting of AC1 and C1.

4. The transgenic plant according to claim 3 in which the geminivirus DNA comprises DNA encoding an amino acid sequence selected from the group consisting of FLTYpxC; pHlHvliQ; vKxYxdKd; FHPNlQxak; EGx_2RTGKt; and NviDDi.

5. The transgenic plant according to claim 1 in which the geminivirus DNA is a transdominant interference mutant of a geminivirus gene.

6. The transgenic plant according to claim 5 in which the geminivirus DNA comprises an ORF selected from the group consisting of AC1 and C1.

7. The transgenic plant according to claim 5 in which the geminivirus DNA encodes a sequence motif select d from the group consisting of a DNA-nicking domain and a NTP-binding domain.

8. The transgenic plant according to claim 7 in which at least one mutation region of the transdominant interference mutant of the geminivirus DNA encodes an amino acid sequence comprising FLTYpxC; pHlHvliQ; vKxYxdKd; FHPNlQxak; EGx$_2$RTGKt; and NviDDi.

9. The transgenic plant according to claims 7 or 8 in which the geminivirus DNA consists of at least one mutation of FLTYpxC; pHlHvliQ; vKxYxdKd; FHPNlQxak; EGx$_2$RTGKt; and NviDDi in the AC1 ORF.

10. The transgenic plant according to claims 7 or 8 in which the geminivirus DNA consists of at least one mutation of FLTYpxC; pHlHvliQ; vKxYxdKd; FHPNlQxak; EGx$_2$RTGKt; and NviDDi.

11. A transgenic plant according to claim 8 in which the geminivirus DNA is a ToMoV AC1 mutant selected from the group consisting of Sequence ID Nos. 3, 5, 7, 13, 14 and 15.

12. A transgenic plant according to claim 8 in which the geminivirus DNA is a TYLCV C1 mutant selected from the group consisting of Sequence ID Nos. 23, 26, and 29.

13. A transgenic plant according to claim 8 in which the geminivirus DNA is a BGMV AC1 mutant selected from the group consisting of Sequence ID Nos. 45, 48, 51, and 54.

14. A method of interfering with geminivirus infection of a transgenic plant comprising:

selecting a transgenic plant according to claim 1; and

growing said transg nic plant.

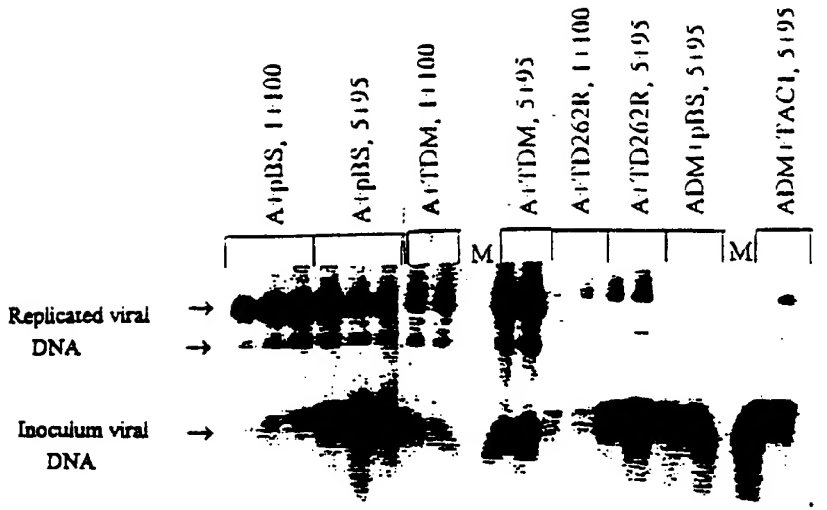
AtpBS, 11100
AtpBS, 5195
AtTDM, 11100
M
AtTDM, 5195
AtTD262R, 11100
AtTD262R, 5195
ADMtpBS, 5195
M
ADMtTAC1, 5195
Replicated viral DNA
Inoculum viral DNA

Fig. 1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/06300

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12N 5/14, 7/04
US CL :435/236; 800/205
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/172.3, 236, 320.1; 800/205

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN, MEDLINE, BIOSIS, EMBASE, WPIDS
search terms: geminivirus, tomato mottel virus, ToMoV, tomato yellow leaf curl virus, TYLCV, transgenic, C1, AC1, motif

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X -- Y	KUNIK et al. Transgenic tomato plants expressing the tomato yellow leaf curl virus capsid protein are resistant to the virus. Bio/Technology. May 1994, Vol. 12, pages 500-504, see entire document.	1-2, 14 ----- 3-13
Y	HANSON et al. Mutational analysis of a putative NTP-binding domain in the replication-associated protein (AC1) of bean golden mosaic geminivirus. Virology. 01 August 1995, Vol. 211, pages 1-9, see entire document.	3-13
X,P --- Y,P	NORIS et al. Resistance to tomato yellow curl geminivirus in Nicotiana benthamiana plants transformed with a truncated viral C1 gene. Virology. 01 October 1996, Vol. 224, pages 130-138, see entire document.	1-3, 5-6, 14 ------- 4, 7-13

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
17 MAY 1997	31 JUL 1997
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer AMY NELSON Telephone No. (703) 308-0196

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/06300

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

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X Y	Database WPIL on Questel, week 9618. Derwent Publications Ltd. AN 96-179947. WO 9608573 (GRONENBORN, B.) 15 September 1995.	1-2, 14 3-13

8. The transgenic plant according to claim 7 in which at least one mutation region of the transdominant interference mutant of the geminivirus DNA encodes an amino acid sequence comprising FLTYpxC; pHlHvliQ; vKxYxdKd; FHPNlQxak; EGx$_2$RTGKt; and NviDDi.

9. The transgenic plant according to claims 7 or 8 in which the geminivirus DNA consists of at least one mutation of FLTYpxC; pHlHvliQ; vKxYxdKd; FHPNlQxak; EGx$_2$RTGKt; and NviDDi in the AC1 ORF.

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13. A transgenic plant according to claim 8 in which the geminivirus DNA is a BGMV AC1 mutant selected from the group consisting of Sequence ID Nos. 45, 48, 51, and 54.

14. A method of interfering with geminivirus infection of a transgenic plant comprising:

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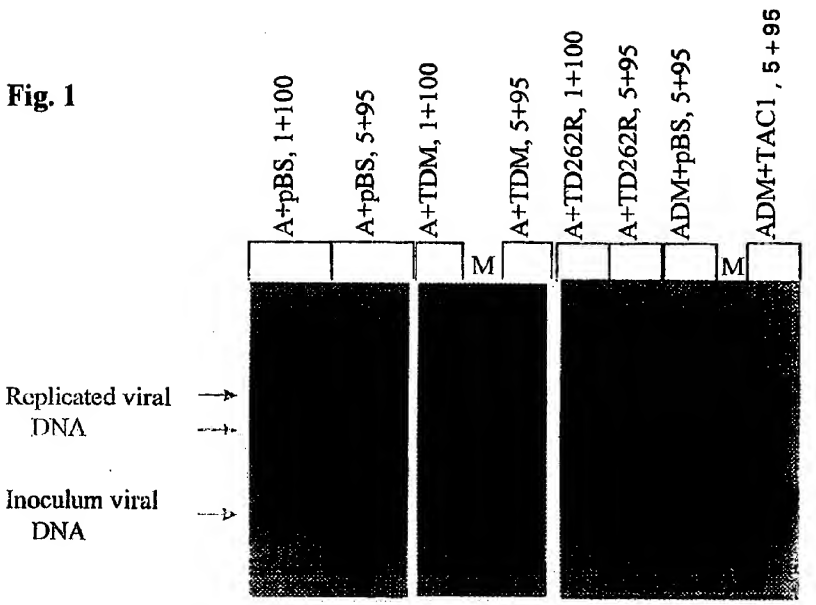
growing said transgenic plant.

Fig. 1


A+pBS, 1+100
A+pBS, 5+95
A+TDM, 1+100
M
A+TDM, 5+95
A+TD262R, 1+100
A+TD262R, 5+95
ADM+pBS, 5+95
M
ADM+TAC1 , 5 + 95
Replicated viral DNA
Inoculum viral DNA

INTERNATIONAL SEARCH REPORT

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PCT/US97/06300

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search terms: geminivirus, tomato mottel virus, ToMöV, tomato yellow leaf curl virus, TYLCV, transgenic, C1, AC1, motif

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Date of the actual completion of the international search	Date of mailing of the international search report
17 MAY 1997	11 JUL 1997

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	AMY NELSON
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

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PCT/US97/06300

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